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[Continued on next page]

(54) Title: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS

Disease-Free
Samples

RCC Samples

	C06A	C07A	C09A	O114_0	O124_0	C01A	C02A	C03A	C04A	O115_0	O119_0	O122_0	O134_0	O135_0	202_1	205_1	209_1	210_1	211_1	302_1	303_1	304_1	401_1	402_1	403_1	404_1	405_1	407_1	410_1	411_1	412_1	413_1	414_1	415_1	501_1	502_1	504_1	505_1	507_1	512_1	513_1	514_1	515_1	518_1	519_1
40310_at																																													
35367_at																																													
35692_at																																													
34666_at																																													
35175_f_at																																													
372587_at																																													
37337_at																																													
329_s_at																																													

(57) Abstract: Methods, systems and equipment for diagnosing renal cell carcinoma (RCC) and other solid tumors. This invention identifies numerous disease genes that are differentially expressed in the peripheral blood of patients having RCC or other solid tumors relative to disease-free humans. These disease genes can be used as surrogate markers for detecting the presence or absence of RCC or other solid tumors.



For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS

[0001] This application incorporates by reference the entire disclosure of U.S. Provisional Application Serial No. 60/427,982, filed November 21, 2002 and entitled "Methods for Diagnosing RCC and/or Solid Tumors." This application also incorporates by reference the entire disclosure of U.S. Provisional Application Serial No. 60/459,782, filed April 3, 2003 and entitled "Methods for Diagnosing RCC and/or Solid Tumors." In addition, this application incorporates by reference all materials recorded in compact discs "Copy 1," "Copy 2," and "Copy 3." Each of the compact discs includes the sequence listing file entitled "AM101080L Sequence Listing.ST25.txt" (2,206 KB, created on November 20, 2003).

TECHNICAL FIELD

[0002] This invention relates to methods, systems and equipment for diagnosing RCC and other solid tumors.

BACKGROUND

[0003] Renal cell carcinoma (RCC) comprises the majority of all cases of kidney cancer and is one of the most common cancers in industrialized countries. When detected early, radical nephrectomy can result in an excellent survival rate for RCC patients. However, the survival rate for patients with metastasized RCC tumors is reduced dramatically. Therefore, there is a need to provide methodologies, systems and equipment for the early diagnosis of RCC.

[0004] RCC patients frequently have non-specific symptoms or are completely asymptomatic. In fact, a significant percentage of renal lesions are incidentally detected by non-invasive imaging techniques. General screening methods for RCC are available, but these methods lack sufficient sensitivity and specificity for broad application. Recent U.S. Patent No. 6,087,098 generally describes an RT-PCR based method for detecting the expression of the MN gene in peripheral blood samples. The MN protein is believed to be a marker of malignant renal cells. Therefore, detection of the MN gene expression in the peripheral blood suggests the presence of RCC.

[0005] The present invention represents a significant advance in the diagnosis of RCC and/or other solid tumors such as prostate cancer and head/neck cancer. The

diagnostic test of the present invention relies on the detection of gene expression patterns in peripheral blood cells rather than in tumor cells themselves. As such, the present invention allows widespread screen for early stages of solid tumor progression.

SUMMARY OF THE INVENTION

[0006] The present invention identifies numerous disease genes that are differentially expressed in the peripheral blood of patients having RCC or other solid tumors as compared to disease-free humans. These disease genes can be used as surrogate markers for detecting the presence or absence of RCC or other solid tumors.

[0007] In accordance with one aspect of the present invention, a method is provided that is useful for diagnosis of RCC and other solid tumors. The method comprises the steps of providing at least one peripheral blood sample of a human, and comparing an expression profile of one or more genes in the at least one peripheral blood sample to at least one reference expression profile of the one or more genes. Each of the one or more genes is differentially expressed in PBMCs of patients having a solid tumor as compared to PBMCs of disease-free humans, provided that if the one or more genes consist of only one gene, the gene is not selected from the group consisting of IL1B, IL6, MMP-9 and FCGR3B, and further provided that if the one or more gene consist of two genes, the two genes are not IL1B and IL6.

[0008] The peripheral blood sample can be a whole blood sample or a sample comprising enriched peripheral blood mononuclear cells (PBMCs). Other peripheral blood samples can also be used. The solid tumor can be, for example, RCC, prostate cancer, or head/neck cancer. The human being investigated can have the solid tumor, or is free from the solid tumor or other diseases.

[0009] The reference expression profile(s) can include an expression profile of the one or more genes in peripheral blood samples of disease-free humans. The reference expression profile(s) can also include an expression profile of the one or more genes in peripheral blood samples of patients having the solid tumor. In addition, the reference expression profile(s) can further include an expression profile of the one or more genes in peripheral blood samples of patients having another solid tumor. The expression profile of the human being investigated can be compared to different reference expression profiles using a weighted voting algorithm.

[0010] The expression profile of the human being investigated and the reference expression profile(s) can be determined using quantitative RT-PCR, Northern Blot, *in situ* hybridization, Southern Blot, slot-blotting, nuclease protection assay, or nucleic acid arrays. The expression profiles can also be determined using immunoassays such as ELISA (enzyme-linked immunosorbent assay), RIA (radioimmunoassay), FACS (fluorescence-activated cell sorter), or Western Blot. In addition, methods based on 2-dimensional SDS-polyacrylamide gel electrophoresis can be used.

[0011] In a preferred embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, or more genes selected from Gene-Table-4. In another preferred embodiment, the one or more genes include at least 1, 2, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, or more genes selected from Table-6. In yet another preferred embodiment, the one or more genes include a classifier identifiable using a two-class or multi-class correlation metric algorithm.

[0012] In still another embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 genes selected from the group consisting of: EEF1A2, TLR2, BRF2, LGALS3, SNRPG, DKFZP586E1621, NUMA1, SOD2, AKR1B1, DUSP6, SMARCE1, KIAA0669, MSF, IL1RN, PTMA, KIAA0410, PSMD3, T54, C1QBP, and OSR1.

[0013] In a further embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 genes selected from the group consisting of: CD44, KIAA0410, MARCO, MAP3K8, NSP-CL, PIP5K1C, NRG1, RAB31, LGALS3, MEF2D, ITGA7, LHFPL2, ETS2, KHSRP, ENIGMA, UNK_AF038187, RAB13, TLR2, T54 and DUSP6.

[0014] In yet another embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 genes selected from the group consisting of: CD44, CRADD, CCRL2, KIAA0837, KIAA0707, KIAA1113, EREG, UNK_AL050119, PPARD, CTSL, ATP2B1, UNK_AF052115, MITF, STAT3, KIAA0410, TPD52L2, UNK_AI732885, MARCO, LOC64116, and PDNP2.

[0015] In still yet another embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, or more genes selected from the group consisting of: FABP5, SCYA20, ADM, COPEB, FCGR3B, UNK_M62896, FN1, HMOX1, ITGA7, DGCR5, CBP2, SLC1A4, MMP9, SLC16A3, LILRB3, FCGR1A, LHFPL2, PLEC1, S100A11, SPOP, CCR1, TLR2 and KIAA0750.

[0016] In another embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, or more genes selected from the group consisting of: ADM, COPEB, AQP9, PTGS2, STIP1, SOD2, PDXK, IL1RN, ANXA5, IFIT4, IL1B, GRO1, PLAUR, NP, MMP9, SLC16A3, LILRB3, FCGR1A, LHFPL2, PLEC1, S100A11, SPOP, CCR1, TLR2, KIAA0750, CDC34, POLR2J, ETS2, MAD, GPR3, PIP5K1C, PRF1, PSMA7, INPP4A, TCFL1, DGAT, S100P, DOC-1R, C8FW, PDI2, GEF-2, TNNT1, BSG, IL17R, HK3, RALBP1, RNASE2, TPM1, BLVRB, APS, PPARD, NFE2, IL1RAP, S100A12, CD9, ENIGMA, HAGH, NCF1, FLOT1, ITGA2B, KIAA0750, FKBP8, DUSP6 and CBFA2T3.

[0017] In yet another embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or more genes selected from the group consisting of: NUMA1, CXCR4, IL10RA, M9, FAU, BRF2, RPS6, EEF1A2, BAG5, AKR1B1, UNK_AL022721, C1QBP, DKZP586E0820, NONO, PSMD3, UNK_N74607, UNK_AI743507, MAPKAPK5, and UNK_U79297.

[0018] In another preferred embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, or more genes, each of which has an RNA transcript capable of hybridizing under stringent conditions to a different respective classification probe sequence (CPS) selected from CPS-Table-2. In one specific example, if the one or more genes consist of only one gene, the RNA transcript(s) of the gene can not hybridize under stringent conditions to a CPS selected from the group consisting of CPSs 58, 211, 221 and 241. In another specific example, if the one or more genes consist of two genes, the RNA transcript(s) of the two genes can not hybridize under stringent conditions to CPSs 211 and 241.

[0019] In one embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 genes, each of which has an RNA transcript capable of hybridizing under stringent conditions to a different respective CPS selected from the group consisting of: CPS 1, CPS 3, CPS 4, CPS 6, CPS 18, CPS 38, CPS 53, CPS 255, CPS 256, CPS 257, CPS 258, CPS 259, CPS 260, CPS 261, CPS 262, CPS 263, CPS 264, CPS 265, CPS 266, and CPS 267.

[0020] In another embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 genes, each of which has an RNA transcript capable of hybridizing under stringent conditions to a different respective CPS selected from the group

consisting of: CPSs 1, 3, 4, 5, 6, 7, 9, 10, 11, 16, 28, 31, 268, 264, 279, 280, 281, 282, 283 and 284.

[0021] In yet another embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or 20 genes, each of which has an RNA transcript capable of hybridizing under stringent conditions to a different respective CPS selected from the group consisting of: CPSs 17, 31, 37, 50, 59, 64, 69, 71, 264, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277 and 278.

[0022] In still yet another embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, or more genes, each of which has an RNA transcript capable of hybridizing under stringent conditions to a different respective CPS selected from the group consisting of: CPSs 1, 2, 8, 16, 19, 26, 28, 57, 58, 61, 91, 92, 99, 138, 143, 148, 152, 191, 192, 207, 221, 229, 236 and 245.

[0023] In yet another embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, or more genes, each of which has an RNA transcript capable of hybridizing under stringent conditions to a different respective CPS selected from the group consisting of: CPSs 1, 4, 9, 10, 11, 12, 14, 17, 18, 19, 21, 25, 28, 34, 35, 40, 47, 52, 53, 58, 61, 62, 84, 87, 91, 92, 94, 99, 104, 105, 109, 111, 115, 125, 128, 130, 133, 135, 138, 143, 146, 147, 148, 151, 154, 157, 158, 165, 173, 174, 178, 191, 192, 194, 195, 201, 211, 220, 222, 227, 244, 247 and 250.

[0024] In one further embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, or more genes, each of which has an RNA transcript capable of hybridizing under stringent conditions to a different respective CPS selected from the group consisting of: CPSs 107, 131, 255, 256, 258, 259, 265, 266, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, and 295.

[0025] In yet another preferred embodiment, the one or more genes include at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, or more genes, each of which has an RNA transcript capable of hybridizing under stringent or nucleic acid array hybridization conditions to a different respective qualifier selected from ATTACHMENT A. In one specific example, if the one or more genes consist of only one gene, the RNA transcript(s) of the gene can not hybridize under stringent or nucleic acid array hybridization conditions to a qualifier selected from the group consisting of 37148_at, 39402_at, 31859_at and 38299_at. In another specific example, if the one or more genes consist of two genes, the

RNA transcript(s) of the two genes can not hybridize under stringent or nucleic acid array hybridization conditions to qualifiers 39402_at and 38299_at.

[0026] In accordance with another aspect of the present invention, a method is provided that is useful for diagnosing or confirming a non-blood disease. The non-blood disease can be a solid tumor such as RCC, prostate cancer, or head/neck cancer. The non-blood disease can also be a non-tumor disease, including diseases capable of causing renal failure. The method includes the steps of providing at least one peripheral blood sample of a human having the non-blood disease, and comparing an expression profile of one or more genes in the at least one peripheral blood sample to at least one reference expression profile of the one or more genes, where each of the one or more genes is differentially expressed in PBMCs of patients having the non-blood disease as compared to PBMCs of disease-free humans.

[0027] In one embodiment, the one or more genes comprise at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, or more genes selected from Gene-Table-4, and the peripheral blood sample is a whole blood sample or a sample comprising enriched PBMCs. In another embodiment, the reference expression profile(s) include an expression profile of the one or more genes in peripheral blood samples of humans who do not have the non-blood disease or are disease-free. In yet another embodiment, the average expression level of each of the one or more genes in PBMCs of patients having the non-blood disease is substantially higher or substantially lower than that in PBMCs of humans who do not have the non-blood disease or are disease-free.

[0028] In accordance with yet another aspect of the present invention, a method is provided that is useful for identifying a gene that is differentially expressed in peripheral blood samples of non-blood disease patients as compared to peripheral blood samples of reference humans. The method comprises the steps of providing an expression profile of one or more genes in peripheral blood samples of non-blood disease patients, providing a reference expression profile of the one or more genes in peripheral blood samples of reference humans, and comparing the expression profile to the reference expression profile to identify a gene that is differentially expressed in non-blood disease patients relative to reference humans. The expression profile and the reference expression profile can be determined, for example, by hybridizing cRNA or cDNA prepared from the peripheral blood samples to one or more nucleic acid arrays. The reference humans can be disease-free humans. The reference humans can also have the non-blood disease but at a different

disease stage or with a different clinical response than the patients being investigated. In one embodiment, the non-blood disease is a solid tumor.

[0029] In accordance with still yet another aspect of the present invention, a kit is provided that is useful for diagnosis of RCC or other solid tumors. In one embodiment, the kit includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, or more polynucleotides, each polynucleotide capable of hybridizing under stringent conditions to an RNA transcript, or the complement thereof, of a different respective gene which is differentially expressed in PBMCs of patients having a solid tumor as compared to PBMCs of disease-free humans. In another embodiment, the kit includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, or more antibodies, each antibody capable of binding to a polypeptide encoded by a different respective gene which is differentially expressed in PBMCs of patients having a solid tumor relative to disease-free humans.

[0030] In accordance with a further aspect of the present invention, a system is provided that is useful for diagnosis of a non-blood disease. The non-blood disease can be a solid tumor, such as RCC, prostate cancer, or head/neck cancer. The system includes a memory which stores one or more reference expression profiles of at least one gene in peripheral blood samples of reference humans. Each gene is differentially expressed in PBMCs of patients having the non-blood disease as compared to PBMCs of disease-free humans. The peripheral blood samples can be whole blood samples or samples comprising enriched PBMCs. The one or more reference expression profiles can include a peripheral blood expression profile of disease-free humans. The one or more reference expression profiles can also include a peripheral blood expression profile of patient having the non-blood disease. In addition, the one or more reference expression profiles can include a peripheral blood expression profile of patients having another non-blood disease. The system further includes a program capable of comparing an expression profile of interest to the one or more reference expression profiles, and a processor capable of executing the program. In one embodiment, the program employs a weighted voting algorithm.

BRIEF DESCRIPTION OF THE DRAWINGS

[0031] This application incorporates by reference the entire disclosure, including all of the drawings, of the U.S. utility patent application filed November 21, 2003 and entitled "Methods for Diagnosing RCC and Other Solid Tumors."

[0032] The drawings are provided for illustration, not limitation.

[0033] FIG. 1 depicts the statistical verification of the RCC disease genes identified in this invention.

[0034] FIG. 2 shows a dendrogram of sample relatedness using expressed gene expression values.

[0035] FIG. 3 is a diagram summarizing the training set cross validation results for predictor gene set of increasing size.

[0036] FIG. 4 illustrates the relative expression levels of a set of eight predictive genes in a training set.

[0037] FIG. 5A demonstrates the cross validation results for each sample in the training set using the 8-gene predictor set as illustrated in FIG. 4.

[0038] FIG. 5B shows the prediction results for the remaining test set of RCC and normal PBMC samples using the 8 gene predictor set as illustrated in FIG. 4.

DETAILED DESCRIPTION

I. DEFINITION

[0039] As used herein, "CPS-Table-2" refers to the entire classification probe sequences (CPSs) listed in Table 2.

[0040] "Gene-Table-4" refers to all of the genes listed in Table 4.

[0041] A "gene" refers to a DNA sequence in the human genome, from which at least one RNA molecule can be transcribed. As used in the present invention, a gene can be a hypothetical or putative gene the expression of which is supported by EST or mRNA data.

[0042] A "disease-free human" refers to a human who does not have any detectable cancer or other diseases which require medical attention or treatment.

[0043] "Stringent conditions" are at least as stringent as, for example, conditions G-L shown in Table 1. "Highly stringent conditions" are at least as stringent as conditions A-F shown in Table 1. As used in Table 1, hybridization is carried out under the hybridization conditions (Hybridization Temperature and Buffer) for about four hours, followed by two 20-minute washes under the corresponding wash conditions (Wash Temp. and Buffer).

Table 1. Stringency Conditions

Stringency Condition	Poly-nucleotide Hybrid	Hybrid Length (bp) ¹	Hybridization Temperature and Buffer ^H	Wash Temp. and Buffer ^H
A	DNA:DNA	>50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
B	DNA:DNA	<50	T _B *; 1xSSC	T _B *; 1xSSC
C	DNA:RNA	>50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
D	DNA:RNA	<50	T _D *; 1xSSC	T _D *; 1xSSC
E	RNA:RNA	>50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
F	RNA:RNA	<50	T _F *; 1xSSC	T _F *; 1xSSC
G	DNA:DNA	>50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
H	DNA:DNA	<50	T _H *; 4xSSC	T _H *; 4xSSC
I	DNA:RNA	>50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
J	DNA:RNA	<50	T _J *; 4xSSC	T _J *; 4xSSC
K	RNA:RNA	>50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
L	RNA:RNA	<50	T _L *; 2xSSC	T _L *; 2xSSC

1: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

^H: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers.

$T_B^* - T_R^*$: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(^{\circ}\text{C}) = 2(\# \text{ of A} + \text{T bases}) + 4(\# \text{ of G} + \text{C bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log_{10}\text{Na}^+) + 0.41(\% \text{G} + \text{C}) - (600/\text{N})$, where N is the number of bases in the hybrid, and Na^+ is the molar concentration of sodium ions in the hybridization buffer (Na^+ for 1xSSC = 0.165M).

[0044] Various aspects of the invention are described in further detail in the following sections and subsections. The use of sections and subsections is not meant to limit the invention; each section and subsection may apply to any aspect of the invention.

II. THE INVENTION

[0045] The present invention provides methods for diagnosing RCC and other solid tumors by detecting gene expression patterns in peripheral blood. The present invention identifies a plurality of RCC disease genes which are differentially expressed in the peripheral blood of RCC patients compared to disease-free humans. At least a subset of these RCC disease genes is also differentially expressed in other solid tumors such as prostate cancer and head/neck cancer. Therefore, these genes can be used as surrogate markers for detecting the presence or absence of RCC and/or other solid tumors. In one embodiment, the expression patterns of these genes in peripheral blood can be determined by assessing the levels of RNA transcripts of these genes in peripheral blood samples. The peripheral blood samples may be the whole blood or blood samples containing enriched PBMCs. Suitable methods for detecting RNA levels include, but are not limited to, quantitative RT-PCT, Northern Blot, *in situ* hybridization, Southern Blot, slot-blotting, nuclease protection assay, and nucleic acid arrays. In another embodiment, the gene expression patterns can be determined by detecting the levels of polypeptides encoded by the solid tumor disease genes. Suitable methods include, but are not limited to, immunoassays such as ELISA (enzyme-linked immunosorbent assay), RIA

(radioimmunoassay), FACS (fluorescence-activated cell sorter), or Western Blot. Methods based on 2-dimensional SDS-polyacrylamide gel electrophoresis can also be used.

A. General Methods for Identifying RCC and Solid Tumor Disease Genes in Peripheral Blood

[0046] The availability of the human genome sequence, together with new developments in technology, such as DNA microarrays, proteomics and computational biology, allows systemic gene expression studies for various diseases. This invention employs the systematic gene expression analysis technique to identify genes and/or markers that are differentially expressed in the peripheral blood of patients with solid tumors such as RCC, prostate cancer, and head/neck cancer. These genes are herein referred to as "solid tumor disease genes." In particular, the genes that are differentially expressed in the peripheral blood of RCC patients compared to disease-free humans are referred to as "RCC disease genes."

[0047] Solid tumor disease genes are either over-expressed or under-expressed (including no expression) in the peripheral blood of solid tumor patients compared to disease-free humans. Therefore, solid tumor disease genes can be identified by comparing the gene expression patterns of solid tumor patients to the corresponding gene expression patterns of disease-free humans. Methods for detecting and comparing gene expression patterns are well known in the art.

[0048] In one embodiment, the gene expression patterns are detected by measuring the levels of RNA transcripts in the peripheral blood. For instance, total RNAs or polyA⁺ RNAs can be isolated from a peripheral blood sample. As used herein, a biological material, such as a polynucleotide, a polypeptide, a cell or a blood sample, is "isolated" if the biological material is removed from its native environment. For instance, a polynucleotide or a polypeptide can be isolated through a purification or extraction process. A blood sample can be isolated when it is removed from the human body.

[0049] The isolated RNAs are then amplified to produce cDNAs or cRNAs. The level of expression of a gene in the peripheral blood sample can be determined by measuring the amount of the corresponding cDNAs or cRNAs thus amplified.

[0050] One exemplary amplification protocol uses reverse transcriptase. For instance, isolated mRNAs can be first reverse transcribed into cDNAs using a reverse

transcriptase, and a primer consisting of oligo d(T) and a sequence encoding the phage T7 promoter. The cDNAs thus produced are single-stranded. The second strands of the cDNAs are synthesized using a DNA polymerase, combined with an RNase to break up the DNA/RNA hybrid. After synthesis of the double-stranded cDNAs, T7 RNA polymerase is added, and cRNAs are then transcribed from the second strands of the doubled-stranded cDNAs.

[0051] In another embodiment, the gene expression patterns can be analyzed by measuring the levels of polypeptides in the peripheral blood. The amounts of polypeptides in a peripheral sample can be detected using various methods well known in the art. Suitable methods include, but are not limited to, immunoassays such as ELISA, RIA, FACS and Western Blot. High-throughput protein sequencing and identification methods can also be used, such as the methods based on two-dimensional gel electrophoresis and mass spectrometry.

[0052] In a preferred embodiment, the peripheral blood samples used for isolating RNA or polypeptides contain enriched or purified peripheral blood mononuclear cells (PBMCs). Methods for preparing blood samples with concentrated PBMCs are well known in the art. For instance, whole blood isolated from human subjects can be centrifuged through Ficoll gradients or CPTs (cell purification tubes), and the fraction containing enriched PBMCs is collected. "Enriched" means that the percentage of PBMCs in the sample is higher than the percentage of PBMCs in the initial whole blood. For instance, the percentage of PBMCs in the enriched sample can be at least 2, 3, 4, 5 or more times higher than that in the initial whole blood. In one embodiment, whole blood can be directly used to screen for solid tumor disease genes.

[0053] In another preferred embodiment, polynucleotide arrays, such as cDNA or oligonucleotide arrays, can be used to detect and/or compare the gene expression profiles in the peripheral blood of solid tumor patients versus disease-free humans. Polynucleotide arrays allow quantitative detecting and monitoring of the levels of RNA transcripts of a large number of genes at one time. Polynucleotide arrays suitable for this global gene expression analysis include, but are not limited to, commercially available arrays such as Genechip® arrays from Affymetrix (Santa Clara, CA) or cDNA microarrays from Agilent Technologies (Palo Alto, CA).

[0054] Polynucleotides to be hybridized to microarrays can be labeled with one or more labeling moieties to allow for detection of hybridized polynucleotide complexes. The

labeling moieties can include compositions that can be detected by spectroscopic, photochemical, biochemical, bioelectronic, immunochemical, electrical, optical or chemical means. The labeling moieties include radioisotopes, chemiluminescent compounds, labeled binding proteins, heavy metal atoms, spectroscopic markers such as fluorescent markers and dyes, magnetic labels, linked enzymes, mass spectrometry tags, spin labels, electron transfer donors and acceptors, and the like. The polynucleotides to be hybridized to the microarrays can be either DNA or RNA.

[0055] Hybridization reactions can be performed in absolute or differential hybridization formats. In the absolute hybridization format, polynucleotides derived from one sample, such as a peripheral blood sample from a RCC patient or a disease-free human, are hybridized to the probes in a microarray. Signals detected after the formation of hybridization complexes correlate to the polynucleotide levels in the sample. In the differential hybridization format, polynucleotides derived from two biological samples, such as one from solid tumor patients and the other from disease-free humans, are labeled with different labeling moieties. A mixture of these differently labeled polynucleotides is added to a microarray. The microarray is then examined under conditions in which the emissions from the two different labels are individually detectable. In one embodiment, the fluorophores Cy3 and Cy5 (Amersham Pharmacia Biotech, Piscataway N.J.) are used as the labeling moieties for the differential hybridization format.

[0056] Signals gathered from microarrays can be analyzed using commercially available software, such as those provide by Affymetrix or Agilent Technologies. Controls, such as for scan sensitivity, probe labeling and cDNA quantitation, preferably are included in the hybridization experiments. The microarray expression signals can be scaled or normalized before being subject to further analysis. For instance, the expression signals for each gene can be normalized to take into account variations in hybridization intensities when more than one array is used under similar test conditions. Signals for individual polynucleotide complex hybridization can also be normalized using the intensities derived from internal normalization controls contained on each array. In addition, genes with relatively consistent expression levels across the samples can be used to normalize the expression levels of other genes. In one embodiment, the expression levels of the genes are normalized across the samples such that the mean is zero and the standard deviation is one. In another embodiment, the expression data detected by the microarray are subject to a

variation filter which excludes genes showing minimal or insignificant variation across all samples.

[0057] The gene expression profiles in the peripheral blood samples of solid tumor patients can be compared to the corresponding gene expression profiles in the peripheral blood samples of disease-free humans. Genes that are differentially expressed in solid tumor patients relative to disease-free humans are identified. Preferably, the level of expression of a solid tumor disease gene is substantially higher or lower in solid tumor patients than in disease-free humans. "Substantially higher" means that the average expression level of a gene in the peripheral blood samples of solid tumor patients is at least 1.5 times over the average expression level of the gene in the peripheral blood samples of disease-free humans. For instance, the average expression level in solid tumor patients can be at least 2, 3, 4, 5, 10, 20, or more times over the average expression level in disease-free humans. "Substantially lower" means that the average expression level of a gene in the peripheral blood samples of solid tumor patients is no greater than 0.67 times over the average expression level of the gene in the peripheral blood samples of disease-free humans. For instance, the average expression level in solid tumor patients can be no greater than 0.5, 0.33, 0.25, 0.1, 0.05 or less times over the average expression level in disease-free humans.

[0058] In one embodiment, solid tumor disease genes can be identified using clustering algorithms based on the microarray gene expression data. For instance, unsupervised cluster analysis can be used to analyze and categorize genes with different expression patterns, thereby identifying solid tumor disease genes. Algorithms for unsupervised cluster analysis include, but are not limited to, self-organized maps (SOMs), principle component analysis, average linkage clustering, and hierarchical clustering.

[0059] Supervised cluster analysis can also be employed to organize and identify solid tumor disease genes. Under supervised cluster analysis, the disease status of the source from which a gene expression pattern is derived is already known. Algorithms for supervised cluster analysis include, but are not limited to, nearest neighbors test, support vector machines, and SPLASH. Either two-class or multi-class correlation metrics can be used.

[0060] In a preferred embodiment, a permutation test-based neighborhood analysis is used to analyze the microarray gene expression data in order to identify solid tumor disease genes. The algorithm for the neighborhood analysis is described in T.R. Golub, *et*

al., Science, 286: 531-537 (1999), and D.K. Slonim *et al.*, Procs. of the Fourth Annual International Conference on Computational Molecular Biology, Tokyo, Japan, April 8 - 11, p263-272 (2000), both of which are incorporated herein by reference.

[0061] Under one form of the neighborhood analysis, the expression profile of each gene is represented by an expression vector $g = (e_1, e_2, e_3, \dots, e_n)$, where e_i corresponds to the expression level of gene "g" in the i th sample. A class distinction is represented by an idealized expression pattern $c = (c_1, c_2, c_3, \dots, c_n)$, where $c_i = 1$ or -1 , depending on whether the i th sample is isolated from class 0 or class 1. Class 0 may consist of patients with a particular solid tumor such as RCC, and class 1 may represent disease-free humans. Class 0 may also consist of patients with different solid tumors.

[0062] The correlation of gene "g" to the class distinction can be calculated using a signal-to-noise score:

$$P(g,c) = \frac{x0(g) - x1(g)}{sd0(g) + sd1(g)}$$

where $x0(g)$ and $x1(g)$ represent the means of the log of the expression level of gene "g" in class 0 and class 1, respectively, and $sd0(g)$ and $sd1(g)$ represent the standard deviation of the log of the expression of gene "g" in class 0 and class 1, respectively. A higher absolute value of a signal-to-noise score indicates that the corresponding gene is more highly expressed in one class than in the other. An unusually high density of genes within the neighborhoods of the class distinction, as compared to random patterns, suggests that many genes have expression patterns that are significantly correlated with the class distinction.

[0063] A plurality of solid tumor disease genes can be selected using the neighborhood analysis. In one embodiment, each solid tumor disease gene thus selected has a substantially higher or lower expression level in PBMCs of solid tumor patients than in PBMCs of disease-free humans. In another embodiment, the selected solid tumor disease genes have top absolute values of $P(g,c)$. In yet another embodiment, the selected solid tumor disease genes include both genes that are highly expressed in class 0 (such as RCC patients), and genes that are highly expressed in class 1 (such as disease-free humans). The solid tumor disease genes selected in the present invention can be involved in different biological pathways or mechanisms.

[0064] In one embodiment, the number of the selected solid tumor disease genes is limited to those shown to be significantly correlated by the permutation test, such as at the

1% or 2% significant level. As used herein, x% significant level means that x% of random neighborhoods contain as many genes as the real neighborhood around the class distinction.

[0065] The general methods for identifying solid tumor disease genes can be used to identify genes whose expression levels in the peripheral blood or PBMCs correlate with different stages of the development, progression or treatment of solid tumors. Patients can be grouped based on their different disease development or treatment stages. The global gene expression analysis can be employed to search for genes that are differentially expressed in one stage compared to another stage. The genes thus identified can be used as markers for monitoring the progression or treatment of solid tumors.

B. Identification of RCC Disease Genes

[0066] In one embodiment, HG-U95Av2 gene chips (manufactured by Affymetrix) are used for detecting and comparing the levels of RNA transcripts in PBMC-enriched peripheral blood samples prepared from RCC patients and disease-free humans. Table 2 lists examples of qualifiers on a HG-U95Av2 gene chip. Each qualifier represents multiple oligonucleotide probes that are stably attached to discrete regions on the gene chip. ATTACHMENT A, which is incorporated herein by reference, lists examples of qualifiers and their corresponding oligonucleotide probes. Each qualifier in Table 2 corresponds to at least one RCC disease gene which is differentially expressed in the peripheral blood of RCC patients compared to disease-free humans. In general, the corresponding RCC disease gene(s) of a qualifier can hybridize under stringent or nucleic acid array hybridization conditions to the oligonucleotide probes listed under the same qualifier in ATTACHMENT A.

[0067] The SEQ ID NO listed under each qualifier in Table 2 depicts a cDNA or genomic sequence, or the complement thereof, of the corresponding RCC disease gene(s). Fragments of the SEQ ID NO can be used to make oligonucleotide probes for detecting the RNA transcripts of the corresponding RCC disease gene(s). ATTACHMENT A includes some examples of the oligonucleotide probes thus made.

[0068] Each SEQ ID NO may have a corresponding Entrez Nucleotide Sequence Database accession number. The SEQ ID NOs and their corresponding accession numbers are illustrated in Table 3. The Entrez Nucleotide Sequence Database is maintained by the National Center of Biotechnology Information (NCBI), National Library of Medicine,

Washington, DC, U.S.A. The Database is publicly known and readily accessible. The Entrez Nucleotide Sequence Database contains sequence data from GenBank, EMBL and DDBJ. The sequence depicted under each SEQ ID NO can be derived from the sequence disclosed under the corresponding Entrez accession number.

[0069] The ambiguous nucleotide residues ("n") in the SEQ ID NOs can be determined using methods as appreciated by one of ordinary skill in the art. For instance, the ambiguous residues can be determined by aligning the SEQ ID NOs to their corresponding genes. The sequences of these genes can be obtained from various human genome sequence databases. The ambiguous nucleotide residues can also be determined by re-sequencing the corresponding SEQ ID NOs or the sequences under the corresponding Entrez accession numbers. Generally, each ambiguous position either represents at least one nucleotide selected from a, c, g, or t, or contains no nucleotide residue.

[0070] Each qualifier has a corresponding classification probe sequence (CPS) which is derived from the SEQ ID NO listed under the same qualifier. The corresponding CPS consists of at least part of the SEQ ID NO, or the complement thereof. Preferably, each CPS does not contain any ambiguous nucleotide residue. More preferably, each CPS comprises at least one oligonucleotide probe listed under the corresponding qualifier in ATTACHMENT A. Each CPS is capable of hybridizing under stringent or highly stringent conditions to the RNA transcripts of the RCC disease gene(s) represented by the corresponding qualifier. All of the CPSs listed in Table 2 are collectively referred to as "CPS-Table-2".

[0071] RNA transcripts, such as mRNAs, can be isolated from PBMC-enriched peripheral blood samples of RCC patients and disease-free humans. cRNAs can then be prepared using protocols described in the Affymetrix's Expression Analysis Technical Manuals. Subsection G of this specification provides detailed examples for sample preparation, HG-U95Av2 genechip hybridization, and subsequent data analysis.

[0072] A hybridization signal is collected for each oligonucleotide probe on the genechip. Signals for oligonucleotide probes with the same qualifier are averaged. Qualifiers that produce different hybridization signals in RCC samples relative to disease-free samples are identified. Examples of the identified qualifiers are listed in Table 2.

[0073] Each RCC expression profile in Table 2 ("Averaged Expression Level in RCC Patients") is an average of 45 RCC patients, while each expression profile for disease-free humans ("Averaged Expression Level in Disease-Free Humans") is an average of 20

disease-free humans. The averaged expression level under each qualifier in Table 2 represents the level of RNA transcripts of the corresponding RCC disease gene(s). The ratio of each RCC expression profile over the corresponding disease-free expression profile is provided under "Fold Change." The p-value of a Student's *t*-test (two-tailed distribution, two sample unequal variance) for each qualifier is also provided. The p-value suggests the statistical significance of the difference between each RCC expression profile and the corresponding disease-free expression profile. Lesser p-values indicate more statistical significance for the differences observed between RCC patients and disease-free humans.

Table 2. Comparison of Gene Expression Levels Between RCC Patients and Disease-Free Humans

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	<i>t</i> -test p-value	Fold Change (RCC/ Disease-Free)
1	40310_at	nucleotides 2325 to 2635 of SEQ ID NO: 1	34.8	13.8	4.8E-10	2.5
2	41126_at	the complement of nucleotides 81 to 523 of SEQ ID NO: 2	5.71	2.7	1.9E-09	2.1
3	35367_at	nucleotides 61 to 865 of SEQ ID NO: 3	107	51.4	2.4E-09	2.1
4	41193_at	nucleotides 2095 to 2390 of SEQ ID NO: 4	26.2	8.2	2.7E-09	3.2
5	38829_r_at	SEQ ID NO: 5	19.7	7.9	5.0E-09	2.5
6	41102_at	nucleotides 1144 to 1607 of SEQ ID NO: 6	8.44	1.95	5.4E-09	4.3
7	40210_at	nucleotides 616 to 1159 of SEQ ID NO: 7	9.89	4.25	2.1E-08	2.3
8	37069_at	nucleotides 847 to 1236 of SEQ ID NO: 8	4.64	2.2	2.9E-08	2.1
9	39530_at	nucleotides 1129 to 1365 of SEQ ID NO: 9	8.51	4.15	3.0E-08	2.05
10	38739_at	nucleotides 46637 to 47224 of SEQ ID NO: 10	6.4	3	3.5E-08	2.1

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
11	32133_at	nucleotides 4460 to 5038 of SEQ ID NO: 11	12.9	4.45	3.7E-08	2.9
12	33873_at	nucleotides 950 to 1324 of SEQ ID NO: 12	15.7	6.9	4.5E-08	2.3
13	39854_r_at	nucleotides 988 to 1568 of SEQ ID NO: 13	34.6	14.05	5.5E-08	2.7
14	38546_at	nucleotides 4101 to 4542 of SEQ ID NO: 14	4.4	2.05	5.6E-08	2.1
15	1856_at	nucleotides 1544 to 1984 of SEQ ID NO: 15	8.47	3.7	5.8E-08	2.3
16	36892_at	nucleotides 3458 to 4037 of SEQ ID NO: 16	4.58	2.25	8.4E-08	2.0
17	37152_at	nucleotides 3047 to 3258 of SEQ ID NO: 17	8.47	3.5	9.9E-08	2.4
18	37603_at	nucleotides 1184 to 1653 of SEQ ID NO: 18	68.1	16.6	1.2E-07	4.1
19	37148_at	nucleotides 2098 to 2157 of SEQ ID NO: 19	41.2	18.25	1.8E-07	2.3
20	34740_at	SEQ ID NO: 20	65.1	22.25	1.8E-07	2.9
21	37747_at	nucleotides 127 to 557 of SEQ ID NO: 21	27.0	13.15	2.0E-07	2.05
22	36567_at	nucleotides 154 to 380 of SEQ ID NO: 22	6.02	2.8	2.1E-07	2.15
23	38956_at	nucleotides 688 to 1225 of SEQ ID NO: 23	4.56	2.1	2.8E-07	2.2
24	32207_at	nucleotides 1399 to 1771 of SEQ ID NO: 24	64.7	19.2	2.9E-07	3.4

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
25	36791_g_at	nucleotides 1002 to 1399 of SEQ ID NO: 25	7.62	3.65	3.0E-07	2.1
26	31684_at	nucleotides 812 to 1206 of SEQ ID NO: 26	5.73	2.85	3.2E-07	2.0
27	1401_g_at	nucleotides 2634 to 2981 of SEQ ID NO: 27	6.73	2.3	3.3E-07	2.9
28	37542_at	nucleotides 3676 to 4193 of SEQ ID NO: 28	8.8	2.35	3.5E-07	3.7
29	37966_at	the complement of nucleotides 34 to 320 of SEQ ID NO: 29	7.29	3.25	3.8E-07	2.2
30	38784_g_at	nucleotides 1231 to 1363 of SEQ ID NO: 30	7.51	2.75	4.1E-07	2.7
31	40331_at	nucleotides 1177 to 1673 of SEQ ID NO: 31	5.29	2	4.2E-07	2.6
32	40371_at	nucleotides 2127 to 2443 of SEQ ID NO: 32	12.0	3.55	4.3E-07	3.4
33	32339_at	the complement of nucleotides 9 to 433 of SEQ ID NO: 33	7.67	3.3	5.2E-07	2.3
34	34435_at	nucleotides 2300 to 2842 of SEQ ID NO: 34	23.4	9.4	6.6E-07	2.5
35	37136_at	nucleotides 1547 to 2068 of SEQ ID NO: 35	4.78	2.2	7.0E-07	2.2
36	37285_at	nucleotides 1344 to 1921 of SEQ ID NO: 36	370	54.1	7.0E-07	6.8
37	37391_at	nucleotides 1022 to 1395 of SEQ ID NO: 37	136	38.45	1.1E-06	3.5
38	35692_at	nucleotides 557 to 1078 of SEQ ID NO: 38	13.6	4.6	1.1E-06	3.0

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
39	38449_at	SEQ ID NO: 39	19.5	4.9	1.1E-06	4.0
40	37002_at	nucleotides 252 to 819 of SEQ ID NO: 40	42.2	11.05	1.2E-06	3.8
41	1139_at	nucleotides 813 to 1383 of SEQ ID NO: 41	10.8	4.95	1.3E-06	2.2
42	1622_at	nucleotides 1830 to 2074 of SEQ ID NO: 42	84.2	39.4	1.4E-06	2.1
43	32606_at	nucleotides 12 to 542 of SEQ ID NO: 43	15.8	7.7	1.4E-06	2.1
44	39436_at	nucleotides 926 to 1154 of SEQ ID NO: 44	82.3	24.3	1.7E-06	3.4
45	40274_at	nucleotides 561 to 736 of SEQ ID NO: 45	8.27	19.5	1.7E-06	0.42
46	37945_at	nucleotides 1179 to 1492 of SEQ ID NO: 46	8.13	3.85	1.9E-06	2.1
47	34255_at	nucleotides 1417 to 1798 of SEQ ID NO: 47	7.47	2.85	2.1E-06	2.6
48	905_at	nucleotides 268 to 814 of SEQ ID NO: 48	103	45.75	2.3E-06	2.3
49	1569_r_at	nucleotides 4183 to 4257 of SEQ ID NO: 49	9.27	4.45	2.5E-06	2.1
50	41125_r_at	SEQ ID NO: 50	5.2	2.2	3.0E-06	2.4
51	35256_at	nucleotides 1781 to 2279 of SEQ ID NO: 51	75.9	28.95	3.0E-06	2.6
52	290_s_at	nucleotides 620 to 1233 of SEQ ID NO: 52	9.38	3.55	3.2E-06	2.6
53	34666_at	nucleotides 755 to 1026 of SEQ ID NO: 53	11.3	4.45	4.0E-06	2.5

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
54	34689_at	nucleotides 713 to 1179 of SEQ ID NO: 54	9.31	2.9	4.0E-06	3.2
55	2090_i_at	nucleotides 2 to 36 of SEQ ID NO: 55	54.4	26.2	4.1E-06	2.1
56	37412_at	nucleotides 1319 to 1692 of SEQ ID NO: 56	8.27	3.25	4.1E-06	2.5
57	39799_at	nucleotides 409 to 662 of SEQ ID NO: 57	24.6	7.2	4.2E-06	3.4
58	31859_at	nucleotides 1756 to 2123 of SEQ ID NO: 58	6.31	2.7	4.6E-06	2.3
59	37661_at	nucleotides 4061 to 4398 of SEQ ID NO: 59	19.5	8.35	4.8E-06	2.3
60	36393_at	nucleotides 806 to 1398 of SEQ ID NO: 60	5.69	2.7	5.0E-06	2.1
61	39994_at	nucleotides 1878 to 2214 of SEQ ID NO: 61	10.0	4	5.1E-06	2.5
62	35597_at	nucleotides 282 to 675 of SEQ ID NO: 62	5.22	2.35	5.3E-06	2.2
63	36780_at	nucleotides 1236 to 1651 of SEQ ID NO: 63	172	79.95	5.7E-06	2.15
64	34476_r_at	nucleotides 4012 to 4358 of SEQ ID NO: 64	11	3.5	5.7E-06	3.1
65	33862_at	nucleotides 1027 to 1445 of SEQ ID NO: 65	3.91	1.85	5.7E-06	2.1
66	956_at	SEQ ID NO: 66	23.0	8.7	5.8E-06	2.6
67	40769_r_at	nucleotides 6070 to 6132 of SEQ ID NO: 67	22.9	10.35	6.3E-06	2.2
68	41790_at	nucleotides 80268 to 80822 of SEQ ID NO: 68	4.2	1.8	6.6E-06	2.3

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
		68				
69	40456_at	nucleotides 733 to 1310 of SEQ ID NO: 69	11.3	5.15	6.8E-06	2.2
70	40647_at	nucleotides 4621 to 5041 of SEQ ID NO: 70	17.4	5.85	7.4E-06	3.0
71	31834_r_at	nucleotides 4249 to 4499 of SEQ ID NO: 71	5.78	2.85	7.8E-06	2.0
72	38119_at	nucleotides 437 to 935 of SEQ ID NO: 72	137	60.95	8.1E-06	2.3
73	1670_at	nucleotides 977 to 1421 of SEQ ID NO: 73	3.62	1.8	8.1E-06	2.0
74	1649_at	nucleotides 384 to 651 of SEQ ID NO: 74	10.5	4.4	8.1E-06	2.4
75	38868_at	nucleotides 205 to 808 of SEQ ID NO: 75	7.82	3.25	9.3E-06	2.4
76	37952_at	nucleotides 3852 to 4432 of SEQ ID NO: 76	13.4	5.25	1.0E-05	2.6
77	654_at	nucleotides 1905 to 2355 of SEQ ID NO: 77	65.4	21.35	1.1E-05	3.1
78	39839_at	nucleotides 1398 to 1568 of SEQ ID NO: 78	70.2	16.3	1.2E-05	4.3
79	41743_i_at	nucleotides 1613 to 2103 of SEQ ID NO: 79	10.4	4.1	1.2E-05	2.5
80	37405_at	nucleotides 1113 to 1429 of SEQ ID NO: 80	140	20.3	1.2E-05	6.9
81	936_s_at	nucleotides 60 to 556 of SEQ ID NO: 81	12.0	3.95	1.3E-05	3.0
82	37323_r_at	nucleotides 130 to 517 of SEQ ID NO: 82	5.09	2.25	1.6E-05	2.3

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
83	33336_at	SEQ ID NO: 83	58.0	7.75	1.7E-05	7.5
84	36229_at	nucleotides 2518 to 2844 of SEQ ID NO: 84	3.84	1.9	1.8E-05	2.0
87	41442_at	nucleotides 3614 to 4179 of SEQ ID NO: 85	8.69	2.55	2.1E-05	3.4
89	33080_s_at	nucleotides 5056 to 5248 of SEQ ID NO: 86	170	51.95	2.1E-05	3.3
90	34742_at	nucleotides 774 to 926 of SEQ ID NO: 87	14.3	3.35	2.2E-05	4.3
91	37026_at	nucleotides 803 to 1325 of SEQ ID NO: 88	54.3	24.9	2.2E-05	2.2
92	34777_at	nucleotides 901 to 1449 of SEQ ID NO: 89	50.3	20.15	2.3E-05	2.5
93	36037_g_at	nucleotides 6396 to 6496 of SEQ ID NO: 90	13	2.35	2.4E-05	5.5
94	40644_g_at	nucleotides 2734 to 2853 of SEQ ID NO: 91	19.7	6.35	2.4E-05	3.1
95	35331_at	nucleotides 2038 to 2395 of SEQ ID NO: 92	5.16	2.2	2.6E-05	2.3
96	875_g_at	nucleotides 562 to 886 of SEQ ID NO: 93	98	14.75	3.2E-05	6.6
97	35773_i_at	the complement of nucleotides 98 to 398 of SEQ ID NO: 94	21.0	5.7	3.3E-05	3.7
98	39802_at	nucleotides 444 to 991 of SEQ ID NO: 95	18.9	5.2	3.4E-05	3.6
99	37220_at	nucleotides 150 to 425 of SEQ ID NO: 96	8.67	4.05	3.9E-05	2.1
100	37192_at	nucleotides 2337 to 2715 of SEQ ID NO: 97	94.8	23.6	3.9E-05	4.0

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
101	31610_at	nucleotides 224 to 512 of SEQ ID NO: 98	18.4	7.95	3.9E-05	2.3
102	37104_at	nucleotides 1227 to 1673 of SEQ ID NO: 99	17.4	2.85	4.0E-05	6.1
103	38582_at	the complement of nucleotides 40 to 288 of SEQ ID NO: 100	5.58	2	4.1E-05	2.8
104	41169_at	nucleotides 890 to 1006 of SEQ ID NO: 101	6.22	2.25	4.2E-05	2.8
105	1274_s_at	nucleotides 741 to 899 of SEQ ID NO: 102	20.6	5.85	4.3E-05	3.5
106	40177_at	the complement of nucleotides 67 to 276 of SEQ ID NO: 103	3.93	1.85	4.6E-05	2.1
107	35659_at	nucleotides 3019 to 3325 of SEQ ID NO: 104	19.2	40.25	4.8E-05	0.48
108	35337_at	nucleotides 1596 to 2056 of SEQ ID NO: 105	124	52.85	4.9E-05	2.3
109	38584_at	nucleotides 1459 to 1700 of SEQ ID NO: 106	9.18	4.45	5.0E-05	2.1
110	1997_s_at	nucleotides 325 to 388 of SEQ ID NO: 107	4.2	8.65	5.2E-05	0.49
111	36162_at	nucleotides 1062 to 1560 of SEQ ID NO: 108	37.2	10.25	5.2E-05	3.6
112	867_s_at	nucleotides 1820 to 1945 of SEQ ID NO: 109	11.3	3.9	5.5E-05	2.9
113	38799_at	nucleotides 2706 to 2791 of SEQ ID NO: 110	7.62	1.85	5.6E-05	4.1
115	36628_at	nucleotides 3321 to 3804 of SEQ ID NO: 111	11.1	5.55	6.2E-05	2.0

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
116	34545_at	nucleotides 1003 to 1158 of SEQ ID NO: 112	8.13	3.65	6.4E-05	2.2
117	31346_at	nucleotides 647 to 1187 of SEQ ID NO: 113	6.64	2.7	6.4E-05	2.5
118	40926_at	nucleotides 13656 to 14081 of SEQ ID NO: 114	18.1	6.8	6.5E-05	2.7
119	33803_at	nucleotides 3479 to 4005 of SEQ ID NO: 115	34.5	16.15	6.8E-05	2.1
120	296_at	SEQ ID NO: 116	15.0	6.55	6.9E-05	2.3
123	41617_at	the complement of nucleotides 41 to 485 of SEQ ID NO: 117	8.42	2.8	8.6E-05	3.0
125	1774_at	nucleotides 497 to 845 of SEQ ID NO: 118	5.93	2.55	8.8E-05	2.3
126	40990_at	nucleotides 1006 to 1405 of SEQ ID NO: 119	8.29	3.45	8.8E-05	2.4
127	34798_at	nucleotides 732 to 1259 of SEQ ID NO: 120	39.8	15.55	8.9E-05	2.6
128	35674_at	nucleotides 3798 to 4194 of SEQ ID NO: 121	6.69	2.9	9.7E-05	2.3
129	1368_at	nucleotides 4459 to 4885 of SEQ ID NO: 122	14.6	6.2	9.8E-05	2.4
130	430_at	nucleotides 444 to 960 of SEQ ID NO: 123	18	8.9	0.00010	2.0
131	39248_at	the complement of nucleotides 55 to 344 of SEQ ID NO: 124	17.8	47	0.00010	0.38
132	33932_at	nucleotides 2013 to 2558 of SEQ ID NO: 125	28.4	10.1	0.00011	2.8

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
133	35767_at	the complement of nucleotides 59 to 621 of SEQ ID NO: 126	60.1	27.55	0.00011	2.2
134	33516_at	SEQ ID NO: 127	149	23.2	0.00011	6.4
135	40120_at	nucleotides 426 to 948 of SEQ ID NO: 128	31.9	7.5	0.00011	4.3
136	31380_at	nucleotides 3015 to 3534 of SEQ ID NO: 129	10.4	4.9	0.00012	2.1
137	35379_at	nucleotides 2491 to 2893 of SEQ ID NO: 130	18.7	7.4	0.00013	2.5
138	38138_at	nucleotides 133 to 574 of SEQ ID NO: 131	28.6	12.15	0.00013	2.4
139	355_s_at	nucleotides 250 to 850 of SEQ ID NO: 132	4.96	2.3	0.00013	2.2
141	36045_at	SEQ ID NO: 133	4.31	1.8	0.00014	2.4
142	39145_at	nucleotides 647 to 1120 of SEQ ID NO: 134	5.98	1.8	0.00016	3.3
143	39423_f_at	nucleotides 1589 to 1642 of SEQ ID NO: 135	6	2.95	0.00017	2.0
144	38598_at	the complement of nucleotides 149 to 213 of SEQ ID NO: 136	8.84	3.5	0.00017	2.5
145	33799_at	nucleotides 1981 to 2240 of SEQ ID NO: 137	29.6	13.85	0.00017	2.1
146	34319_at	nucleotides 39 to 419 of SEQ ID NO: 138	22.9	9.55	0.00017	2.4
147	36113_s_at	nucleotides 14630 to 14687 of SEQ ID NO: 139	4.13	2.05	0.00019	2.0
148	40848_g_at	nucleotides 3447 to 3808 of SEQ ID NO: 140	14.6	2.95	0.00019	4.9

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
149	2094_s_at	nucleotides 2713 to 3294 of SEQ ID NO: 141	66.6	136	0.00020	0.49
150	37185_at	nucleotides 1311 to 1761 of SEQ ID NO: 142	226	84.55	0.00020	2.7
151	35714_at	nucleotides 642 to 960 of SEQ ID NO: 143	7.71	3.2	0.00021	2.4
152	40951_at	nucleotides 1860 to 2099 of SEQ ID NO: 144	5.27	2.3	0.00022	2.3
153	37187_at	nucleotides 504 to 946 of SEQ ID NO: 145	59.1	19.55	0.00023	3.0
154	33506_at	nucleotides 2672 to 3121 of SEQ ID NO: 146	7.07	2.2	0.00023	3.2
155	34430_at	nucleotides 2931 to 3119 of SEQ ID NO: 147	12.6	6.1	0.00025	2.1
156	40062_s_at	SEQ ID NO: 148	9.36	2.35	0.00027	4.0
157	37179_at	nucleotides 1069 to 1648 of SEQ ID NO: 149	10.1	3.15	0.00028	3.2
158	1486_at	nucleotides 145 to 529 of SEQ ID NO: 150	5.22	1.8	0.00028	2.9
159	40182_s_at	nucleotides 1849 to 2085 of SEQ ID NO: 151	5.73	2.7	0.00029	2.1
160	36419_at	nucleotides 850 to 1028 of SEQ ID NO: 152	4.22	1.8	0.00029	2.3
161	32581_at	SEQ ID NO: 153	4.24	2	0.00035	2.1
162	31308_at	nucleotides 36 to 484 of SEQ ID NO: 154	4	1.8	0.00039	2.2
163	36871_at	nucleotides 2087 to 2652 of SEQ ID NO: 155	14.2	2.55	0.00037	5.5

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
164	40956_at	nucleotides 2649 to 3183 of SEQ ID NO: 156	12.9	5.25	0.00038	2.45
165	35151_at	nucleotides 436 to 895 of SEQ ID NO: 157	4.18	1.9	0.00039	2.2
166	39543_at	the complement of nucleotides 106 to 619 of SEQ ID NO: 158	7.51	3.3	0.00041	2.3
167	725_i_at	nucleotides 1844 to 2146 of SEQ ID NO: 159	11.5	29.8	0.00043	0.39
168	31454_f_at	nucleotides 878 to 972 of SEQ ID NO: 160	5.6	2.55	0.00047	2.2
169	40366_at	nucleotides 2709 to 3063 of SEQ ID NO: 161	13.5	4.4	0.00048	3.1
170	1251_g_at	nucleotides 3043 to 3230 of SEQ ID NO: 162	8.53	2.45	0.00048	3.5
171	115_at	nucleotides 3083 to 3605 of SEQ ID NO: 163	42.2	17.25	0.00049	2.4
172	34447_at	nucleotides 2881 to 3318 of SEQ ID NO: 164	6.58	2.35	0.00050	2.8
173	38879_at	nucleotides 19 to 325 of SEQ ID NO: 165	40.0	17.25	0.00050	2.3
174	39389_at	nucleotides 686 to 1058 of SEQ ID NO: 166	14.9	7.4	0.00054	2.0
175	39729_at	nucleotides 712 to 968 of SEQ ID NO: 167	25.4	8.4	0.00057	3.0
176	39448_r_at	nucleotides 46 to 468 of SEQ ID NO: 168	8.07	16.45	0.00058	0.49
177	33759_at	nucleotides 1090 to 1582 of SEQ ID NO: 169	17.0	5	0.00059	3.4
178	33449_at	nucleotides 893 to 969 of SEQ ID NO: 170	10.5	5	0.00060	2.1

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
179	31812_at	nucleotides 1047 to 1464 of SEQ ID NO: 171	32.2	12.55	0.00061	2.6
180	40578_s_at	nucleotides 2081 to 2425 of SEQ ID NO: 172	12.1	2.45	0.00078	4.9
181	40766_at	SEQ ID NO: 173	11.4	4.25	0.00079	2.7
182	31320_at	nucleotides 631 to 1169 of SEQ ID NO: 174	3.84	1.8	0.00081	2.1
183	34378_at	nucleotides 1217 to 1314 of SEQ ID NO: 175	102	28.2	0.00092	3.6
184	40773_at	nucleotides 37 to 522 of SEQ ID NO: 176	9.56	3.15	0.0010	3.0
185	38726_at	the complement of nucleotides 125 to 494 of SEQ ID NO: 177	20.8	3.6	0.0010	5.8
186	1832_at	nucleotides 3598 to 4132 of SEQ ID NO: 178	5.00	2.05	0.0010	2.4
187	36543_at	nucleotides 1723 to 2013 of SEQ ID NO: 179	6.87	1.95	0.0011	3.5
188	137_at	nucleotides 1138 to 1564 of SEQ ID NO: 180	6.02	1.8	0.0012	3.3
189	38585_at	SEQ ID NO: 181	258	74.25	0.0012	3.5
190	34022_at	nucleotides 426 to 993 of SEQ ID NO: 182	32.2	4.25	0.0012	7.6
191	38021_at	nucleotides 14286 to 14757 of SEQ ID NO: 183	5.67	2.25	0.0013	2.5
192	33143_s_at	nucleotides 1523 to 1918 of SEQ ID NO: 184	18.7	6.1	0.0015	3.1
194	40850_at	nucleotides 1048 to 1504 of SEQ ID NO:	16.9	4.1	0.0016	4.1

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/Disease-Free)
		185				
195	36766_at	nucleotides 167 to 666 of SEQ ID NO: 186	24.5	11.3	0.0017	2.2
196	38201_at	nucleotides 836 to 1155 of SEQ ID NO: 187	7.18	3.05	0.0018	2.4
199	2092_s_at	nucleotides 824 to 1229 of SEQ ID NO: 188	9.78	2.35	0.0022	4.2
201	408_at	nucleotides 1229 to 1851 of SEQ ID NO: 189	21.1	2.4	0.0028	8.8
202	36058_at	nucleotides 1083 to 1550 of SEQ ID NO: 190	29.6	11.7	0.0030	2.5
205	38429_at	nucleotides 7939 to 8395 of SEQ ID NO: 192	5.00	2.4	0.0035	2.1
206	502_s_at	nucleotides 1959 to 2156 of SEQ ID NO: 193	5.18	1.85	0.0041	2.8
207	33802_at	nucleotides 51072 to 51587 of SEQ ID NO: 194	21.4	10.25	0.0047	2.1
208	38010_at	nucleotides 1044 to 1494 of SEQ ID NO: 195	6.58	3.25	0.0050	2.0
209	41046_s_at	nucleotides 5551 to 6046 of SEQ ID NO: 196	4.76	2.2	0.0068	2.2
210	39095_at	nucleotides 5774 to 5945 of SEQ ID NO: 197	5.87	1.8	0.0072	3.3
211	39402_at	nucleotides 927 to 1473 of SEQ ID NO: 198	71.6	18.45	0.0073	3.9
212	37184_at	nucleotides 1631 to 2037 of SEQ ID NO: 199	6.36	2.7	0.0074	2.4

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
213	38273_at	nucleotides 1251 to 1576 of SEQ ID NO: 200	6.47	2.5	0.0075	2.6
214	35894_at	nucleotides 1736 to 2016 of SEQ ID NO: 201	4.67	1.8	0.0076	2.6
215	33429_at	nucleotides 937 to 1538 of SEQ ID NO: 202	6.38	2.6	0.0083	2.5
216	558_at	nucleotides 5446 to 5866 of SEQ ID NO: 203	36.8	11.3	0.0084	3.3
217	41575_at	nucleotides 2056 to 2530 of SEQ ID NO: 204	5.09	2.15	0.0086	2.4
218	39780_at	nucleotides 2550 to 3078 of SEQ ID NO: 205	5.2	2.6	0.0094	2
219	1257_s_at	nucleotides 2590 to 2840 of SEQ ID NO: 206	33.6	14.35	0.0095	2.3
220	32904_at	SEQ ID NO: 207	8.78	20.85	0.0096	0.42
221	31499_s_at	nucleotides 251 to 854 of SEQ ID NO: 208	16.0	6.6	0.010	2.4
222	1069_at	nucleotides 8872 to 9184 of SEQ ID NO: 209	7.82	2.95	0.011	2.7
223	39413_at	nucleotides 6717 to 6771 of SEQ ID NO: 210	4.91	1.8	0.012	2.7
224	34281_at	nucleotides 1207 to 1559 of SEQ ID NO: 211	9.4	3.4	0.012	2.8
225	33914_r_at	SEQ ID NO: 212	19.6	2.15	0.012	9.1
226	35762_at	nucleotides 4753 to 5179 of SEQ ID NO: 213	8.89	2.8	0.013	3.2

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
227	36372_at	nucleotides 2437 to 3029 of SEQ ID NO: 214	6.78	2.95	0.013	2.3
228	32451_at	nucleotides 1020 to 1387 of SEQ ID NO: 215	6.31	1.95	0.013	3.2
229	40385_at	nucleotides 207 to 742 of SEQ ID NO: 216	6.93	2.35	0.014	3.0
230	35036_at	nucleotides 2895 to 3261 of SEQ ID NO: 217	5.4	2.1	0.014	2.6
231	34014_f_at	nucleotides 664 to 1000 of SEQ ID NO: 218	8.38	2.15	0.015	3.9
232	37120_at	nucleotides 1870 to 2379 of SEQ ID NO: 219	12.2	3.45	0.016	3.5
234	32054_at	nucleotides 1916 to 2038 of SEQ ID NO: 220	6.13	2.3	0.017	2.7
235	33742_f_at	nucleotides 248 to 367 of SEQ ID NO: 221	8.09	1.8	0.019	4.5
236	31719_at	nucleotides 7039 to 7633 of SEQ ID NO: 222	3.64	1.8	0.020	2.0
237	35418_at	nucleotides 471 to 714 of SEQ ID NO: 223	11.8	1.85	0.021	6.4
239	1407_g_at	nucleotides 1768 to 1958 of SEQ ID NO: 224	7.11	2.95	0.022	2.4
240	31666_f_at	nucleotides 62 to 339 of SEQ ID NO: 225	13.8	1.8	0.024	7.7
241	38299_at	nucleotides 728 to 1053 of SEQ ID NO: 226	23.9	3	0.025	8.0
242	40517_at	nucleotides 5232 to 5667 of SEQ ID NO: 227	7.84	3.05	0.025	2.6
243	1350_at	nucleotides 2099 to 2350 of SEQ ID NO:	7.8	2.85	0.026	2.7

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
		228				
244	207_at	nucleotides 1512 to 2082 of SEQ ID NO: 229	9.07	3.45	0.028	2.6
245	39166_s_at	nucleotides 1583 to 1790 of SEQ ID NO: 230	8.42	2.75	0.030	3.1
246	31574_i_at	nucleotides 39 to 78 of SEQ ID NO: 231	16.8	1.8	0.034	9.3
247	40159_r_at	nucleotides 970 to 1341 of SEQ ID NO: 232	20.2	8.7	0.035	2.3
248	33244_at	SEQ ID NO: 233	9.29	3.75	0.037	2.5
249	2041_i_at	nucleotides 3736 to 3773 of SEQ ID NO: 234	66.5	2.35	0.038	28
250	40635_at	nucleotides 1460 to 1771 of SEQ ID NO: 235	12.9	5.5	0.039	2.3
251	38908_s_at	nucleotides 2043 to 2283 of SEQ ID NO: 236	20.3	5.65	0.039	3.6
252	732_f_at	SEQ ID NO: 237	21.4	8.5	0.042	2.5
253	32579_at	nucleotides 5059 to 5246 of SEQ ID NO: 238	40.1	7.75	0.043	5.2
254	33021_at	nucleotides 1744 to 1878 of SEQ ID NO: 239	8.42	4.2	0.047	2.0
255	35175_f_at	nucleotides 1252 to 1447 of SEQ ID NO: 285	118.47	191.35	4.4E-10	0.62
256	32587_at	nucleotides 4939 to 5425 of SEQ ID NO: 286	61.16	117.80	5.2E-10	0.52
257	37337_at	the complement of nucleotides 7 to 362 of	14.04	23.55	5.2E-10	0.60

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
		SEQ ID NO: 287				
258	329_s_at	SEQ ID NO: 288	8.44	16.00	3.0E-10	0.53
259	36589_at	nucleotides 797 to 1192 of SEQ ID NO: 289	15.78	23.25	1.7E-08	0.68
260	33828_at	SEQ ID NO: 328	13.07	20.10	6.7E-08	0.65
261	41787_at	the complement of nucleotides 77 to 413 of SEQ ID NO: 291	6.04	3.50	2.1E-08	1.73
262	41220_at	nucleotides 3638 to 3874 of SEQ ID NO: 292	169.69	227.65	3.8E-07	0.75
263	38590_r_at	nucleotides 575 to 1111 of SEQ ID NO: 293	201.78	274.50	1.4E-07	0.74
264	40018_at	nucleotides 5780 to 6213 of SEQ ID NO: 294	7.84	4.45	2.4E-07	1.76
265	39155_at	nucleotides 1548 to 2085 of SEQ ID NO: 295	19.22	25.80	3.9E-08	0.75
266	37668_at	nucleotides 600 to 948 of SEQ ID NO: 296	10.80	17.95	2.9E-11	0.60
267	39136_at	nucleotides 4031 to 4415 of SEQ ID NO: 297	15.33	10.55	3.7E-06	1.45
268	1125_s_at	nucleotides 43 to 226 of SEQ ID NO: 298	8.42	4.50	5.7E-08	1.87
269	1211_s_at	nucleotides 972 to 1076 of SEQ ID NO: 299	7.02	3.80	4.5E-07	1.85
270	1445_at	nucleotides 1097 to 1643 of SEQ ID NO: 300	6.47	3.55	3.6E-07	1.82
271	32405_at	nucleotides 5804 to 6242 of SEQ ID NO: 301	7.69	4.50	2.9E-07	1.71

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
272	32635_at	nucleotides 3240 to 3424 of SEQ ID NO: 302	8.00	4.65	6.9E-05	1.72
273	36331_at	nucleotides 2550 to 3110 of SEQ ID NO: 303	6.42	3.30	7.2E-07	1.95
274	37788_at	nucleotides 1293 -1655 of SEQ ID NO: 304	4.62	2.35	1.2E-05	1.97
275	38228_g_at	nucleotides 1878 to 2045 of SEQ ID NO: 305	6.53	4.25	5.4E-05	1.54
276	39708_at	SEQ ID NO: 306	32.13	19.65	9.5E-08	1.64
277	40076_at	nucleotides 1683 to 2285 of SEQ ID NO: 307	59.36	35.35	2.5E-07	1.68
278	40177_at	the complement of nucleotides 67 to 276 of SEQ ID NO: 308	3.93	1.85	4.6E-05	2.13
279	1891_at	nucleotides 2144 to 2738 of SEQ ID NO: 309	9.16	4.65	1.3E-08	1.97
280	31536_at	nucleotides 3430 to 4018 of SEQ ID NO: 310	25.56	15.75	1.2E-08	1.62
281	32719_at	nucleotides 1261 to 1780 of SEQ ID NO: 311	7.16	4.05	9.6E-08	1.77
282	33371_s_at	nucleotides 420 to 879 of SEQ ID NO: 312	21.31	11.05	8.6E-09	1.93
283	35434_at	nucleotides 1591 to 1897 of SEQ ID NO: 313	12.62	7.25	1.7E-08	1.74
284	40167_s_at	nucleotides 1405 to 1643 of SEQ ID NO: 314	9.11	6.45	3.3E-06	1.41
285	649_s_at	nucleotides 1038 to 1632 of SEQ ID NO: 317	172.87	266.70	3.1E-06	0.65

CPS No.	Qualifier	CPS	Averaged Expression Level in RCC Patients (n = 45)	Averaged Expression Level in Disease-Free Humans (n = 20)	t-test p-value	Fold Change (RCC/ Disease-Free)
286	31492_at	nucleotides 255 to 758 of SEQ ID NO: 318	47.91	64.10	9.7E-09	0.75
287	31955_at	nucleotides 1 to 475 of SEQ ID NO: 319	316.33	435.15	1.4E-08	0.73
288	35125_at	SEQ ID NO: 330	404.47	547.05	5.1E-07	0.74
289	36463_at	nucleotides 3746 to 4119 of SEQ ID NO: 321	13.49	20.05	1.7E-09	0.67
290	36786_at	SEQ ID NO: 329	204.07	304.40	1.1E-09	0.67
291	38269_at	nucleotides 1235 to 1699 of SEQ ID NO: 323	27.64	40.25	3.9E-07	0.69
292	38527_at	nucleotides 2145 to 2484 of SEQ ID NO: 324	53.49	70.70	6.8E-09	0.76
293	40610_at	SEQ ID NO: 331	12.56	20.50	2.7E-06	0.61
294	41506_at	nucleotides 1440 to 1952 of SEQ ID NO: 326	8.11	13.45	2.7E-07	0.60
295	41604_at	nucleotides 1095 to 1400 of SEQ ID NO: 327	13.60	21.30	3.5E-07	0.64

Table 3. SEQ ID NOs and the Corresponding Entrez Accession Numbers

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
1	AF051152	Homo sapiens Toll/interleukin-1 receptor-like protein 4 (TIL4) mRNA
2	AA978353	
3	AB006780	Homo sapiens mRNA for galectin-3
4	AB013382	Homo sapiens mRNA for DUSP6
6	U66359	Human T54 protein (T54) mRNA
7	X75593	Homo sapiens mRNA for rab 13
8	X91348	Homo sapiens predicted non coding cDNA (DGCR5)

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
9	L35240	Human <i>enigma</i> gene
10	AF017257	Homo sapiens chromosome 21 derived BAC containing erythroblastosis virus oncogene homolog 2 protein (<i>ets-2</i>) gene
11	AB011161	Homo sapiens mRNA for KIAA0589 protein
12	D43642	Human YL-1 mRNA for YL-1 protein (nuclear protein with DNA-binding ability)
13	AF055000	Homo sapiens clone 24519 unknown mRNA
14	AB006537	Homo sapiens mRNA for interleukin 1 receptor accessory protein
15	X75042	Homo sapiens <i>rel</i> proto-oncogene mRNA
16	AF032108	Homo sapiens integrin alpha-7 mRNA
17	L07592	Human peroxisome proliferator activated receptor mRNA
18	X52015	Homo sapiens mRNA for interleukin-1 receptor antagonist
19	AF025533	Homo sapiens leukocyte immunoglobulin-like receptor-3 (LIR-3) mRNA
21	U05770	Human annexin V (ANX5) gene, exon 13
22	W26700	
23	AF052111	Homo sapiens clone 23953 mRNA sequence
24	M64925	Human palmitoylated erythrocyte membrane protein (MPP1) mRNA
25	M19267	Human tropomyosin mRNA
26	M62896	Human lipocortin (LIP) 2 pseudogene mRNA
27	M13207	Human granulocyte-macrophage colony-stimulating factor (CSF1) gene
28	D86961	Human mRNA for KIAA0206 gene
29	AA187563	
30	J05581	Human polymorphic epithelial mucin (PEM) mRNA
31	AF035819	Homo sapiens macrophage receptor MARCO mRNA
32	X51362	Human mRNA for dopamine D2 receptor
33	AA844998	
34	AB008775	Homo sapiens AQP9 mRNA for aquaporin 9
35	AB000520	Homo sapiens mRNA for APS
36	X60364	Human ALAS mRNA for 5-aminolevulinate synthase precursor
37	X12451	Human mRNA for pro-cathepsin L (major excreted protein MEP)
38	AL080235	Homo sapiens mRNA; cDNA DKFZp586E1621 (from clone DKFZp586E1621)
40	D32143	Human mRNA for biliverdin-IXbeta reductase I
41	L22075	Homo sapiens guanine nucleotide regulatory protein (G13) mRNA

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
42	D87116	Human mRNA for MAP kinase kinase 3b
43	AA135683	
44	AF079221	Homo sapiens BCL2/adenovirus E1B 19kDa-interacting protein 3a mRNA
45	U48213	Human D-site binding protein gene, exon 4
46	U91316	Human acyl-CoA thioester hydrolase mRNA
47	AF059202	Homo sapiens ACAT related gene product 1 mRNA
48	L76200	Human guanylate kinase (GUK1) mRNA
49	L42243	Homo sapiens (clone 51H8) alternatively spliced interferon receptor (IFNAR2) gene, exon 9
50	D45421	Human mRNA for phosphodiesterase I alpha
51	AL096737	Homo sapiens mRNA; cDNA DKFZp434F152 (from clone DKFZp434F152)
52	L32831	Homo sapiens G protein-coupled receptor (GPR3) gene
53	X07834	Human mRNA for manganese superoxide dismutase (EC 1.15.1.1)
54	AJ243797	Homo sapiens mRNA for deoxyribonuclease III (drn3 gene)
55	H12458	
56	S78798	1-phosphatidylinositol-4-phosphate 5-kinase isoform C [human, peripheral blood leukocytes, mRNA, 1835 nt]
57	M94856	Human fatty acid binding protein homologue (PA-FABP) mRNA
58	J05070	Human type IV collagenase mRNA
59	J04027	Human plasma membrane Ca ²⁺ pumping ATPase mRNA
60	U43843	Human h-neuro-d4 protein mRNA
61	D10925	Human mRNA for HM145
62	AJ000480	Homo sapiens mRNA for C8FW phosphoprotein
63	M25915	Human complement cytolysis inhibitor (CLI) mRNA
64	D30783	Homo sapiens mRNA for epiregulin
65	AF017786	Homo sapiens phosphatidic acid phosphohydrolase homolog (Dri42) mRNA
66	X79535	Homo sapiens mRNA for beta tubulin, clone nuk 278
67	D14689	Human mRNA for KIAA0023 gene
68	AL031230	Human DNA sequence from clone 73M23 on chromosome 6p22.2-22.3; contains the 5' part of the possibly alternatively spliced gene for Phosphatidylinositol-glycan-specific Phospholipase D 1 precursor (EC 3.1.4.50, PIGPLD1, Glycoprotein Phospholipase D, Glycosyl-Phosphatidylinositol specific Phospholipase D), the gene for NAD+

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
		dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24), and the 3' part of the KIAA0319 gene; contains ESTs, STSs, GSSs and a putative CpG island, complete sequence
69	AL049963	Homo sapiens mRNA; cDNA DKFZp564A132 (from clone DKFZp564A132)
70	Z32684	Homo sapiens mRNA for membrane transport protein (XK gene)
71	AB020644	Homo sapiens mRNA for KIAA0837 protein
72	X12496	Human mRNA for erythrocyte membrane sialoglycoprotein beta (glycophorin C)
73	L23959	Homo sapiens E2F-related transcription factor (DP-1) mRNA
74	U61836	Human putative cyclin G1 interacting protein mRNA
75	U43774	Human Fc alpha receptor, splice variant FcalphaR a.2 (CD89) mRNA
76	M35999	Human platelet glycoprotein IIIa (GPIIIa) mRNA
77	L07648	Human MXI1 mRNA
78	M24069	Human DNA-binding protein A (dbpA) gene, 3' end
79	AF061034	Homo sapiens FIP2 alternatively translated mRNA
80	U29091	Homo sapiens selenium-binding protein (hSBP) mRNA
81	U68111	Human protein phosphatase inhibitor 2 (PPP1R2) gene, exon 6
82	X82460	Homo sapiens mRNA for 15-hydroxy prostaglandin dehydrogenase
84	U58917	Homo sapiens IL-17 receptor mRNA
85	AB010419	Homo sapiens mRNA for MTG8-related protein MTG16a
86	AB007943	Homo sapiens mRNA for KIAA0474 protein
87	Z23115	Homo sapiens bcl-xL mRNA
88	AF001461	Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA
89	D14874	Homo sapiens mRNA for adrenomedullin precursor
90	J05500	Human beta-spectrin (SPTB) mRNA
91	M34480	Human platelet glycoprotein IIb (GPIIb) mRNA
92	U97067	Homo sapiens alpha-catenin-like protein mRNA
93	M26683	Human interferon gamma treatment inducible mRNA
94	AA527880	
95	X72308	Homo sapiens mRNA for monocyte chemotactic protein-3 (MCP-3)
96	M63835	Human IgG Fc receptor I gene, exon 6

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
97	U28389	Human dematin 52 kDa subunit mRNA
98	U21049	Homo sapiens DD96 mRNA
99	L40904	Homo sapiens peroxisome proliferator activated receptor gamma (PPARG) mRNA
100	AI961220	
101	X74039	Homo sapiens mRNA for urokinase plasminogen activator receptor
102	L22005	Human ubiquitin conjugating enzyme mRNA
103	AI732885	
104	U00672	Human interleukin-10 receptor mRNA
105	AL050254	Novel human gene mapping to chromosome 22
106	AF026939	Homo sapiens CIG49 (cig49) mRNA
107	U19599	Human (BAX delta) mRNA
108	X64364	Homo sapiens mRNA for M6 antigen
109	U12471	Human thrombospondin-1 gene
110	AF068706	Homo sapiens gamma2-adaptin (G2AD) mRNA
111	L42542	Human RLIP76 protein mRNA
112	AF070587	Homo sapiens clone 24741 mRNA sequence
113	AJ001481	Homo sapiens mRNA for DUX1 protein
114	U36341	Human Xq28 cosmid, creatine transporter (SLC6A8) gene, complete cds, and CDM gene, partial cds
115	J02973	Human thrombomodulin gene
116	AF141349	Homo sapiens beta-tubulin mRNA
117	AI349593	
118	L06895	Homo sapiens antagonist of myc transcriptional activity (Mad) mRNA
119	AF065389	Homo sapiens tetraspan NET-4 mRNA
120	Z35491	Homo sapiens mRNA for novel glucocorticoid receptor-associated protein
121	AB023211	Homo sapiens mRNA for KIAA0994 protein
122	M27492	Human interleukin 1 receptor mRNA
123	X00737	Human mRNA for purine nucleoside phosphorylase (PNP; EC 2.4.2.1)
124	N74607	
125	X17644	Human GST1-Hs mRNA for GTP-binding protein
126	AI565760	
128	X90999	Homo sapiens mRNA for Glyoxalase II
129	AF059198	Homo sapiens protein kinase/endoribonuclease (IRE1) mRNA
130	X54412	Human mRNA for alpha1(IX) collagen (long form)
131	D38583	Human mRNA for calgizzarin

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
132	D38037	Human mRNA for FK506-binding protein 12kDa (hFKBP-12) homologue
134	J02854	Human 20-kDa myosin light chain (MLC-2) mRNA
135	AJ000644	Homo sapiens mRNA for SPOP
136	AI679353	
137	U76248	Human hSIAH2 mRNA
138	AA131149	
139	AJ011712	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
140	AB018293	Homo sapiens mRNA for KIAA0750 protein
141	K00650	Human fos proto-oncogene (c-fos)
142	Y00630	Human mRNA for Arg-Serpin (plasminogen activator-inhibitor 2, PAI-2)
143	U89606	Human pyridoxal kinase mRNA
144	AL049250	Homo sapiens mRNA; cDNA DKFZp564D113 (from clone DKFZp564D113)
145	M36820	Human cytokine (GRO-beta) mRNA
146	U96919	Homo sapiens inositol polyphosphate 4-phosphatase type I-beta mRNA
147	U70732	Human glutamate pyruvate transaminase (GPT) gene
149	S77763	nuclear factor erythroid 2 isoform f, basic leucine zipper protein {alternatively spliced, exon 1f} [human, fetal liver, mRNA, 1678 nt]
150	L37127	Homo sapiens RNA polymerase II mRNA
151	AF055027	Homo sapiens clone 24658 mRNA sequence
152	AF038171	Homo sapiens clone 23671 mRNA sequence
154	L17330	Human pre-T/NK cell associated protein (6H9A) mRNA
155	M60298	Human erythrocyte membrane protein band 4.2 (EPB42) mRNA
156	X90857	Homo sapiens mRNA for -14 gene, containing globin regulatory element
157	AF089814	Homo sapiens growth suppressor related (DOC-1R) mRNA
158	AI077476	
159	K02401	Human chorionic somatomammotropin gene hCS-1
160	AF034209	Homo sapiens RIG-like 5-6 mRNA
161	M25322	Human granule membrane protein-140 mRNA
162	M64788	Human GTPase activating protein (rap1GAP) mRNA
163	X14787	Human mRNA for thrombospondin
164	U62433	Human nicotinic acetylcholine receptor alpha4 subunit precursor, mRNA
165	D83664	Human mRNA for CAAF1 (calcium-binding protein in amniotic fluid 1)

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
166	M38690	Human CD9 antigen mRNA
167	L19185	Human natural killer cell enhancing factor (NKEFB) mRNA
168	W27095	
169	X04327	Human erythrocyte 2,3-bisphosphoglycerate mutase mRNA EC 2.7.5.4
170	AF054185	Homo sapiens proteasome subunit HSPC mRNA
171	M24470	Human glucose-6-phosphate dehydrogenase
172	M77016	Human tropomodulin mRNA
174	U18548	Human GPR12 G protein coupled-receptor gene
175	X97324	Homo sapiens mRNA for adipophilin
176	L03785	Human regulatory myosin light chain (MYL5) mRNA
177	W80399	
178	M62397	colorectal mutant cancer protein mRNA
179	J02931	Human placental tissue factor (two forms) mRNA
180	U65404	Human erythroid-specific transcription factor EKLF mRNA
182	M36821	Human cytokine (GRO-gamma) mRNA
183	U53204	Human plectin (PLEC1) mRNA
184	U81800	Homo sapiens monocarboxylate transporter (MCT3) mRNA
185	L37033	Human FK-506 binding protein homologue (FKBP38) mRNA
186	X55988	Human EDN mRNA for eosinophil derived neurotoxin
187	U21551	Human ECA39 mRNA
188	J04765	Human osteopontin mRNA
189	X54489	Human gene for melanoma growth stimulatory activity (MGSA)
190	AL096741	Homo sapiens mRNA; cDNA DKFZp586O0223 (from clone DKFZp586O0223)
192	U29344	Human breast carcinoma fatty acid synthase mRNA
193	U37431	Human HOXA1 mRNA, long transcript and alternatively spliced forms
194	Z82244	Human DNA sequence from clone CTA-286B10 on chromosome 22; contains the 3' end of the TOM1 gene for target of myb1 (chicken) homolog, the HMOX1 gene for Heme Oxygenase (decycling) 1 (HO-1, EC 1.14.99.3), the MCM5 gene for minichromosome maintenance deficient (<i>S. cerevisiae</i>) 5 (cell division cycle 46, DNA Replication Licensing Factor, P1-CDC46), ESTs, STSs, GSSs, and two putative CpG islands
195	AF002697	Homo sapiens E1B 19K/Bcl-2-binding protein Nip3

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
		mRNA, nuclear gene encoding mitochondrial protein
196	X95808	Homo sapiens mRNA for protein encoded by a candidate gene, DXS6673E, for mental retardation
197	M58018	Homo sapiens beta-myosin heavy chain (MYH7) mRNA
198	M15330	Human interleukin 1-beta (IL1B) mRNA
199	L37792	Homo sapiens syntaxin 1A mRNA
200	AJ006268	Homo sapiens mRNA for putative ATPase
201	X14362	Human CR1 mRNA for C3b/C4b receptor secreted form
202	AL050225	Homo sapiens mRNA; cDNA DKFZp586M1523 (from clone DKFZp586M1523)
203	M98776	Human keratin 1 gene
204	AF070571	Homo sapiens clone 24739 mRNA sequence
205	M29551	Human calcineurin A2 mRNA
206	L42379	Homo sapiens bone-derived growth factor (BPGF-1) mRNA
208	X16863	Human Fc-gamma RIII-1 cDNA for Fc-gamma receptor III-1 (CD 16)
209	U04636	Human cyclooxygenase-2 (hCox-2) gene
210	AJ001189	Homo sapiens mRNA for oligophrenin 1
211	AF039555	Homo sapiens visinin-like protein 1 (VSNL1) mRNA
213	AB007952	Homo sapiens mRNA for KIAA0483 protein
214	U51333	Human hexokinase III (HK3) mRNA
215	L35848	Homo sapiens IgE receptor beta chain (HTm4) mRNA
216	U64197	Homo sapiens chemokine exodus-1 mRNA
217	U94333	Human Clq/MBL/SPA receptor ClqR(p) mRNA
218	D10216	Human mRNA for Pit-1/GHF-1
219	X91817	Homo sapiens mRNA for transketolase-like protein (2418 bp)
220	AF048732	Homo sapiens cyclin T2b mRNA
221	W27838	
222	X02761	Human mRNA for fibronectin (FN precursor)
223	J04178	Human abnormal beta-hexosaminidase alpha chain (HEXA) mRNA, chromosome 15q23-q24
224	M21985	Human steroid receptor TR2 mRNA
225	W28731	
226	X04430	Human IFN-beta 2a mRNA for interferon-beta-2
227	AB002370	Human mRNA for KIAA0372 gene
228	U02388	Homo sapiens cytochrome P450 4F2 (CYP4F2) mRNA
229	M86752	Human transformation-sensitive protein (IEF SSP 3521) mRNA

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
230	D83174	Human mRNA for collagen binding protein 2
231	M14087	Human HL14 gene encoding beta-galactoside-binding lectin, 3' end, clone 2
232	M55067	Human 47-kD autosomal chronic granulomatous disease protein mRNA
234	M14752	Human c-abl gene
235	AF089750	Homo sapiens flotillin-1 mRNA
236	AL096744	Homo sapiens mRNA; cDNA DKFZp566H033 (from clone DKFZp566H033)
237	M55406	Human intestinal mucin (MUC-3) mRNA
238	U29175	Human transcriptional activator (BRG1) mRNA
239	AF035314	Homo sapiens clone 23651 mRNA sequence
285	X70940	H.sapiens mRNA for elongation factor 1 alpha-2
286	U07802	Human Tis11d gene
287	AI803447	
288	Z11584	Homo sapiens mRNA for NuMA protein
289	X15414	Human mRNA for aldose reductase (EC 1.1.1.2
290	AF035262	Homo sapiens BAF57 (BAF57) gene
291	AI452442	
292	AB023208	Homo sapiens mRNA for KIAA0991 protein
293	M14630	Human prothymosin alpha mRNA
294	AB007870	Homo sapiens KIAA0410 mRNA
295	D67025	Homo sapiens mRNA for proteasome subunit p58
296	M69039	Human pre-mRNA splicing factor SF2p32
297	AB017642	Homo sapiens mRNA for oxidative-stress responsive1
298	L05424	Human cell surface glycoprotein CD44 (CD44) gene, exon 14
299	U84388	Human death domain containing protein CRADD mRNA
300	AF014958	Homo sapiens chemokine receptor X (CKRX) mRNA
301	AB014607	Homo sapiens mRNA for KIAA0707 protein
302	AB029036	Homo sapiens mRNA for KIAA1113 protein
303	AL050119	Homo sapiens mRNA; cDNA DKFZp586C091
304	AF052115	Homo sapiens clone 23688 mRNA sequence
305	AB006909	Homo sapiens mRNA for A-type microphthalmia associated transcription factor
307	AF004430	Homo sapiens hD54+ins2 isoform (hD54) mRNA
308	AI732885	
309	D14497	Human mRNA for proto-oncogene protein
310	AB020693	Homo sapiens mRNA for KIAA0886 protein
311	L41827	Homo sapiens sensory and motor neuron derived factor (SMDF) mRNA,
312	U59877	Human low-Mr GTP-binding protein (RAB31)

SEQ ID NO	Corresponding Entrez Database Accession No.	Reported Source of the Corresponding Entrez Sequence
		mRNA
313	L16794	Human transcription factor (MEF2) mRNA
314	AF038187	Homo sapiens clone 23714 mRNA sequence
315	L29277	Homo sapiens DNA-binding protein (APRF) mRNA
317	L06797	Human (clone L5) orphan G protein-coupled receptor mRNA
318	AB019392	Homo sapiens mRNA of muscle specific gene M9
319	X65923	Homo sapiens fau mRNA
320	X67309	Homo sapiens gene for ribosomal protein S6
321	AB020680	Homo sapiens mRNA for KIAA0873 protein
322	AL022721	Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3, which contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a putative ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). It also contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism.
323	AL050147	Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820)
324	U02493	Human 54 kDa protein mRNA
325	AI743507	wf72a06.x2 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361106 3' similar to TR:O88532 O88532 ZINC FINGER RNA BINDING PROTEIN
326	AF032437	Homo sapiens mitogen activated protein kinase activated protein kinase gene
327	U79297	Human clone 23589 mRNA sequence

[0074] Each qualifier in Table 2 represents at least one RCC disease gene which is differentially expressed in the peripheral blood of RCC patients relative to disease-free humans. The RNA transcripts of the RCC disease gene can hybridize to the corresponding qualifier under stringent or nucleic acid array hybridization conditions. As used herein, "hybridize to a qualifier" means to hybridize to at least one oligonucleotide probe listed under the qualifier in ATTACHMENT A. For instance, the RNA transcripts of the RCC disease gene can hybridize under stringent or nucleic acid array hybridization conditions to at least 2, 4, 6, 8, 10, 12, 14 or 16 oligonucleotide probes listed under the corresponding qualifier in ATTACHMENT A. The RNA transcripts of the RCC disease gene can also

hybridize under stringent or highly stringent conditions to the CPS of the corresponding qualifier.

[0075] RCC disease genes represented by the qualifiers and CPSs of Table 2 can be determined based on the HG-U95Av2 gene chip annotation provided by Affymetrix. They can also be determined based on the Entrez accession numbers listed in Table 3, as appreciated by one of ordinary skill in the art. In addition, the identity of the RCC disease genes can be assessed by BLAST searching the corresponding CPSs or oligonucleotide probes, such as those listed in Table 2 or ATTACHMENT A, against a human genome sequence database. Suitable human genome sequence databases for this purpose include, but are not limited to, the Entrez human genome database maintained at the NCBI. The Entrez human genome database contains about 97.8% of the total human genome sequence, and among them, about 63% are finished sequence and about 34.8% are unfinished sequence. The NCBI provides publicly accessible BLAST programs, such as "blastn," for BLAST searching its sequence database.

[0076] Each CPS aligns with the protein-coding strand(s) of the corresponding RCC disease gene(s). Preferably, each CPS aligns to the corresponding RCC disease gene(s) with at least 97% sequence identity. Each CPS can hybridize to the corresponding RCC disease gene(s) under stringent or highly stringent conditions. Table 4 lists the CPSs and their corresponding RCC disease genes. All of the genes listed in Table 4 are collectively referred to as "Gene-Table 4."

Table 4. RCC Disease Genes

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
1	TLR2	AF051152 (SEQ ID NO: 1); and SEQ ID NO: 240
2	SLC1A4	the complement of AA978353 (SEQ ID NO: 2)
3	LGALS3	AB006780 (SEQ ID NO: 3)
4	DUSP6	AB013382 (SEQ ID NO: 4); and SEQ ID NO: 241
5	KHSRP	SEQ ID NO: 5; and the complement of AA628946 (SEQ ID NO: 242)
6	T54	U66359 (SEQ ID NO: 6)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
7	RAB13	X75593 (SEQ ID NO: 7)
8	DGCR5	X91348 (SEQ ID NO: 8)
9	ENIGMA	L35240 (SEQ ID NO: 9)
10	ETS2	AF017257 (SEQ ID NO: 10); and J04102 (SEQ ID NO: 243)
11	PIP5K1C	AB011161 (SEQ ID NO: 11)
12	TCFL1	D43642 (SEQ ID NO: 12); and SEQ ID NO: 244
13	UNK_AF055000	AF055000 (SEQ ID NO: 13)
14	IL1RAP	AB006537 (SEQ ID NO: 14)
15	REL	X75042 (SEQ ID NO: 15)
16	ITGA7	AF032108 (SEQ ID NO: 16)
17	PPARD	L07592 (SEQ ID NO: 17)
18	IL1RN	X52015 (SEQ ID NO: 18)
19	LILRB3	AF025533 (SEQ ID NO: 19)
20	FOXO3A	SEQ ID NO: 20; and AF032886 (SEQ ID NO: 245)
21	ANXA5	U05770 (SEQ ID NO: 21)
22	SLC17A7 (UNK_W26700)	W26700 (SEQ ID NO: 22)
23	LOC51172 (UNK_AF052111 or APAA)	AF052111 (SEQ ID NO: 23)
24	MPP1	M64925 (SEQ ID NO: 24)
25	TPM1	M19267 (SEQ ID NO: 25)
26	UNK_M62896	M62896 (SEQ ID NO: 26)
27	CSF2	M13207 (SEQ ID NO: 27)
28	LHFPL2	D86961 (SEQ ID NO: 28) (3676-4193)
29	PARVB (UNK_AA187563)	the complement of AA187563 (SEQ ID NO: 29)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
30	MUC1	J05581 (SEQ ID NO: 30)
31	MARCO	AF035819 (SEQ ID NO: 31)
32	DRD2	X51362 (SEQ ID NO: 32)
33	PPY	the complement of AA844998 (SEQ ID NO: 33)
34	AQP9	AB008775 (SEQ ID NO: 34)
35	APS	AB000520 (SEQ ID NO: 35)
36	ALAS2	X60364 (SEQ ID NO: 36)
37	CTSL	X12451 (SEQ ID NO: 37)
38	DKFZP586E1621	AL080235 (SEQ ID NO: 38)
39	PRO2389 (UNK W28931)	SEQ ID NO: 39; and the complement of W28931 (SEQ ID NO: 246)
40	BLVRB	D32143 (SEQ ID NO: 40)
41	GNA13	L22075 (SEQ ID NO: 41)
42	MAP2K3	D87116 (SEQ ID NO: 42)
43	BASP1	AA135683 (SEQ ID NO: 43)
44	BNIP3L	AF079221 (SEQ ID NO: 44)
45	DBP	U48213 (SEQ ID NO: 45)
46	HBACH	U91316 (SEQ ID NO: 46); and SEQ ID NO: 247
47	DGAT	AF059202 (SEQ ID NO: 47)
48	GUK1	L76200 (SEQ ID NO: 48)
49	IL10RB	L42243 (SEQ ID NO: 49)
50	PDNP2	D45421 (SEQ ID NO: 50)
51	SLC5A6 (UNK AL096737)	AL096737 (SEQ ID NO: 51)
52	GPR3	L32831 (SEQ ID NO: 52)
53	SOD2	X07834 (SEQ ID NO: 53); and SEQ ID NO: 248

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
54	TREX1	AJ243797 (SEQ ID NO: 54)
55	WNT6 (UNK_H12458)	H12458 (SEQ ID NO: 55)
56	PIP5K2A (UNK_S78798)	S78798 (SEQ ID NO: 56)
57	FABP5	M94856 (SEQ ID NO: 57); and SEQ ID NO: 249
58	MMP9	J05070 (SEQ ID NO: 58)
59	ATP2B1	J04027 (SEQ ID NO: 59); and SEQ ID NO: 250
60	NEUD4	U43843 (SEQ ID NO: 60)
61	CCR1	D10925 (SEQ ID NO: 61); and SEQ ID NO: 251
62	C8FW	AJ000480 (SEQ ID NO: 62); and SEQ ID NO: 252
63	CLU	M25915 (SEQ ID NO: 63); and SEQ ID NO: 253
64	EREG	D30783 (SEQ ID NO: 64)
65	PPAP2B	AF017786 (SEQ ID NO: 65) SEQ ID NO: 254
66	TUBB	X79535 (SEQ ID NO: 66)
67	NUP214	D14689 (SEQ ID NO: 67)
68	ALDH5A1	AL031230 (SEQ ID NO: 68)
69	LOC64116 (also referred to as UNK_AL049963)	AL049963 (SEQ ID NO: 69)
70	XK	Z32684 (SEQ ID NO: 70)
71	KIAA0837	AB020644 (SEQ ID NO: 71)
72	GYPC	X12496 (SEQ ID NO: 72)
73	TFDP1	L23959 (SEQ ID NO: 73); and W28479 (SEQ ID NO: 255)
74	C20orf16 (UNK_U61836)	U61836 (SEQ ID NO: 74)
75	FCAR	U43774 (SEQ ID NO: 75)
76	ITGB3	M35999 (SEQ ID NO: 76)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
77	MXI1	L07648 (SEQ ID NO: 77); and D63940 (SEQ ID NO: 256)
78	CSDA	M24069 (SEQ ID NO: 78); and SEQ ID NO: 257
79	FIP2	AF061034 (SEQ ID NO: 79)
80	SELENBP1	U29091 (SEQ ID NO: 80); and SEQ ID NO: 258
81	PPP1R2	U68111 (SEQ ID NO: 81)
82	HPGD	X82460 (SEQ ID NO: 82)
83	SLC4A1	SEQ ID NO: 83; and M27819 (SEQ ID NO: 259)
84	IL17R	U58917 (SEQ ID NO: 84)
87	CBFA2T3	AB010419 (SEQ ID NO: 85)
89	RAP1GA1 (KIAA0474)	AB007943 (SEQ ID NO: 86)
90	BCL2L1	Z23115 (SEQ ID NO: 87); and SEQ ID NO: 260
91	COPEB	AF001461 (SEQ ID NO: 88)
92	ADM	D14874 (SEQ ID NO: 89); and SEQ ID NO: 261
93	SPTB	J05500 (SEQ ID NO: 90)
94	ITGA2B	M34480 (SEQ ID NO: 91)
95	CTNNAL1 (UNK U97067)	U97067 (SEQ ID NO: 92)
96	SCYA2	M26683 (SEQ ID NO: 93); and M28225 (SEQ ID NO: 262)
97	NDUFB7	the complement of AA527880 (SEQ ID NO: 94)
98	SCYA7	X72308 (SEQ ID NO: 95)
99	FCGR1A	M63835 (SEQ ID NO: 96); and SEQ ID NO: 263
100	EPB49	U28389 (SEQ ID NO: 97)
101	DD96	U21049 (SEQ ID NO: 98)
102	PPARG	L40904 (SEQ ID NO: 99)
103	SPINK1	the complement of AI961220 (SEQ ID NO: 100)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
		100)
104	PLAUR	X74039 (SEQ ID NO: 101)
105	CDC34	L22005 (SEQ ID NO: 102)
106	UNK_AI732885	the complement of AI732885 (SEQ ID NO: 103)
107	IL10RA	U00672 (SEQ ID NO: 104)
108	FBX7	AL050254 (SEQ ID NO: 105)
109	IFIT4	AF026939 (SEQ ID NO: 106)
110	BAX	U19599 (SEQ ID NO: 107)
111	BSG	X64364 (SEQ ID NO: 108)
112	THBS1 (UNK U12471)	U12471 (SEQ ID NO: 109)
113	G2AD	AF068706 (SEQ ID NO: 110)
115	RALBP1	L42542 (SEQ ID NO: 111)
116	UNK_AF070587 (LOC196932)	AF070587 (SEQ ID NO: 112)
117	DUX1	AJ001481 (SEQ ID NO: 113)
118	SLC6A8	U36341 (SEQ ID NO: 114)
119	THBD	J02973 (SEQ ID NO: 115)
120	UNK_AF141349 (Tubulin, Beta)	AF141349 (SEQ ID NO: 116)
123	HBE1	the complement of AI349593 (SEQ ID NO: 117); and SEQ ID NO: 264
125	MAD	L06895 (SEQ ID NO: 118)
126	TSPAN-5	AF065389 (SEQ ID NO: 119)
127	BAG1	Z35491 (SEQ ID NO: 120)
128	PDI2	AB023211 (SEQ ID NO: 121)
129	IL1R1	M27492 (SEQ ID NO: 122)
130	NP	X00737 (SEQ ID NO: 123)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
131	AQP3 (UNK_N74607)	the complement of N74607 (SEQ ID NO: 124)
132	GSPT1	X17644 (SEQ ID NO: 125)
133	GEF-2	the complement of AI565760 (SEQ ID NO: 126)
134	HBD	SEQ ID NO: 127; and V00505 (SEQ ID NO: 265)
135	HAGH	X90999 (SEQ ID NO: 128)
136	ERN1	AF059198 (SEQ ID NO: 129)
137	COL9A1	X54412 (SEQ ID NO: 130)
138	S100A11	D38583 (SEQ ID NO: 131)
139	FKBP1B	D38037 (SEQ ID NO: 132)
141	RNAH	SEQ ID NO: 133 AJ223948 (SEQ ID NO: 266)
142	MYRL2	J02854 (SEQ ID NO: 134)
143	SPOP	AJ000644 (SEQ ID NO: 135)
144	SLC11A1 (UNK_AI679353)	the complement of AI679353 (SEQ ID NO: 136)
145	SLAH2	U76248 (SEQ ID NO: 137); and SEQ ID NO: 267
146	S100P	AA131149 (SEQ ID NO: 138)
147	TNNT1	AJ011712 (SEQ ID NO: 139); SEQ ID NO: 268; and M19309 (SEQ ID NO: 269)
148	KIAA0750	AB018293 (SEQ ID NO: 140)
149	FOS	K00650 (SEQ ID NO: 141)
150	PAI2	Y00630 (SEQ ID NO: 142)
151	PDXK	U89606 (SEQ ID NO: 143)
152	UNK_AL049250	AL049250 (SEQ ID NO: 144)
153	GRO2	M36820 (SEQ ID NO: 145)
154	INPP4A	U96919 (SEQ ID NO: 146)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
155	GPT	U70732 (SEQ ID NO: 147)
156	MYL4	SEQ ID NO: 148; and X58851 (SEQ ID NO: 270)
157	NFE2	S77763 (SEQ ID NO: 149)
158	POLR2J	L37127 (SEQ ID NO: 150)
159	CARM1	AF055027 (SEQ ID NO: 151)
160	UNK_AF038171	AF038171 (SEQ ID NO: 152)
161	RAB2	SEQ ID NO: 153; and AF070629 (SEQ ID NO: 271)
162	6H9A	L17330 (SEQ ID NO: 154)
163	EPB42	M60298 (SEQ ID NO: 155); and SEQ ID NO: 272
164	CGTHBA	X90857 (SEQ ID NO: 156)
165	DOC-1R	AF089814 (SEQ ID NO: 157)
166	KIAA0353	the complement of AI077476 (SEQ ID NO: 158)
167	CSH1	SEQ ID NO: 159
168	LOC51048	AF034209 (SEQ ID NO: 160)
169	SELP	M25322 (SEQ ID NO: 161)
170	RAP1GA1	M64788 (SEQ ID NO: 162)
171	THBS1	X14787 (SEQ ID NO: 163)
172	CHRNA4	U62433 (SEQ ID NO: 164)
173	S100A12	D83664 (SEQ ID NO: 165)
174	CD9	M38690 (SEQ ID NO: 166)
175	TDPX1	L19185 (SEQ ID NO: 167)
176	B7	W27095 (SEQ ID NO: 168)
177	BPGM	X04327 (SEQ ID NO: 169)
178	PSMA7	AF054185 (SEQ ID NO: 170); and SEQ ID NO: 273

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
179	GMPR	M24470 (SEQ ID NO: 171); and SEQ ID NO: 274
180	TMOD	M77016 (SEQ ID NO: 172)
181	C4A	SEQ ID NO: 173; and U24578 (SEQ ID NO: 275), such as nucleotides 16881 to 16928 and nucleotides 17131-17239 of SEQ ID NO: 275
182	GPR12	U18548 (SEQ ID NO: 174)
183	ADFP	X97324 (SEQ ID NO: 175); and SEQ ID NO: 276
184	MYL5	L03785 (SEQ ID NO: 176)
185	DPM2	the complement of W80399 (SEQ ID NO: 177)
186	MCC	M62397 (SEQ ID NO: 178)
187	F3	J02931 (SEQ ID NO: 179)
188	KLF1	U65404 (SEQ ID NO: 180)
189	HBG2	SEQ ID NO: 181; and M91036 (SEQ ID NO: 277), such as nucleotides 2162-2268, 2391-2614 or 3501-3565 of SEQ ID NO: 277
190	GRO3	M36821 (SEQ ID NO: 182)
191	PLEC1	U53204 (SEQ ID NO: 183)
192	SLC16A3	U81800 (SEQ ID NO: 184)
194	FKBP8	L37033 (SEQ ID NO: 185)
195	RNASE2	X55988 (SEQ ID NO: 186)
196	BCAT1	U21551 (SEQ ID NO: 187); and SEQ ID NO: 278
199	SPP1	J04765 (SEQ ID NO: 188); and AF052124 (SEQ ID NO: 279)
201	GRO1	X54489 (SEQ ID NO: 189)
202	DKFZP586O0223	AL096741 (SEQ ID NO: 190)
205	FASN	U29344 (SEQ ID NO: 192)
206	HOXA1	U37431 (SEQ ID NO: 193)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
207	HMOX1	Z82244 (SEQ ID NO: 194)
208	BNIP3	AF002697 (SEQ ID NO: 195)
209	ZNF261	X95808 (SEQ ID NO: 196)
210	MYH7	M58018 (SEQ ID NO: 197)
211	IL1B	M15330 (SEQ ID NO: 198); and SEQ ID NO: 191
212	STX1A	L37792 (SEQ ID NO: 199)
213	ATPASEP	AJ006268 (SEQ ID NO: 200); and SEQ ID NO: 280
214	CR1	X14362 (SEQ ID NO: 201)
215	DKFZP586M1523	AL050225 (SEQ ID NO: 202)
216	KRT1	M98776 (SEQ ID NO: 203)
217	UNK_AF070571 (EXT1)	AF070571 (SEQ ID NO: 204)
218	PPP3CB	M29551 (SEQ ID NO: 205)
219	QSCN6	L42379 (SEQ ID NO: 206)
220	PRF1	SEQ ID NO: 207 M28393 (SEQ ID NO: 281)
221	FCGR3B	X16863 (SEQ ID NO: 208)
222	PTGS2	U04636 (SEQ ID NO: 209)
223	OPHN1	AJ001189 (SEQ ID NO: 210)
224	VSNL1	AF039555 (SEQ ID NO: 211)
225	FECH	SEQ ID NO: 212; and D00726 (SEQ ID NO: 282)
226	KIAA0483	AB007952 (SEQ ID NO: 213)
227	HK3	U51333 (SEQ ID NO: 214)
228	MS4A3	L35848 (SEQ ID NO: 215)
229	SCYA20	U64197 (SEQ ID NO: 216)
230	C1QR1	U94333 (SEQ ID NO: 217)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
231	POU1F1	D10216 (SEQ ID NO: 218); and D12892 (SEQ ID NO: 283)
232	TKTL1	X91817 (SEQ ID NO: 219)
234	CCNT2	AF048732 (SEQ ID NO: 220)
235	ATP6V1H (UNK_W27838)	W27838 (SEQ ID NO: 221)
236	FN1	X02761 (SEQ ID NO: 222)
237	UNK_J04178 (HEXA)	J04178 (SEQ ID NO: 223)
239	NR2C1	M21985 (SEQ ID NO: 224)
240	KIAA0168	W28731 (SEQ ID NO: 225)
241	IL6	X04430 (SEQ ID NO: 226)
242	KIAA0372	AB002370 (SEQ ID NO: 227)
243	CYP4F2	U02388 (SEQ ID NO: 228)
244	STIP1	M86752 (SEQ ID NO: 229)
245	CBP2	D83174 (SEQ ID NO: 230)
246	UNK_M14087	M14087 (SEQ ID NO: 231)
247	NCF1	M55067 (SEQ ID NO: 232)
248	CHN2	SEQ ID NO: 233; and U07223 (SEQ ID NO: 284)
249	ABL1	M14752 (SEQ ID NO: 234)
250	FLOT1	AF089750 (SEQ ID NO: 235)
251	REV3L (UNK_AL096744)	AL096744 (SEQ ID NO: 236)
252	MUC3	M55406 (SEQ ID NO: 237)
253	SMARCA4	U29175 (SEQ ID NO: 238)
254	LOC92684 (UNK_AF035314)	AF035314 (SEQ ID NO: 239)
255	EEF1A2	X70940 (SEQ ID NO: 285)
256	BRF2	U07802 (SEQ ID NO: 286)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
257	SNRPG	the complement of AI803447 (SEQ ID NO: 287)
258	NUMA1	Z11584 (SEQ ID NO: 288)
259	AKR1B1	X15414 (SEQ ID NO: 289)
260	SMARCE1	AF035262 (SEQ ID NO: 290); and SEQ ID NO: 328
261	KIAA0669	the complement of AI452442 (SEQ ID NO: 291)
262	MSF	AB023208 (SEQ ID NO: 292)
263	PTMA	M14630 (SEQ ID NO: 293)
264	KIAA0410	AB007870 (SEQ ID NO: 294)
265	PSMD3	D67025 (SEQ ID NO: 295)
266	C1QBP	M69039 (SEQ ID NO: 296)
267	OSR1	AB017642 (SEQ ID NO: 297)
268	CD44	L05424 (SEQ ID NO: 298)
269	CRADD	U84388 (SEQ ID NO: 299)
270	CCRL2	AF014958 (SEQ ID NO: 300)
271	KIAA0707	AB014607 (SEQ ID NO: 301)
272	KIAA1113	AB029036 (SEQ ID NO: 302); and SEQ ID NO: 316
273	UNK_AL050119	AL050119 (SEQ ID NO: 303)
274	UNK_AF052115	AF052115 (SEQ ID NO: 304)
275	MITF	AB006909 (SEQ ID NO: 305)
276	STAT3	SEQ ID NO: 306; and L29277 (SEQ ID NO: 315)
277	TPD52L2	AF004430 (SEQ ID NO: 307)
278	UNK_AI732885	the complement of AI732885 (SEQ ID NO: 308)
279	MAP3K8	D14497 (SEQ ID NO: 309)
280	NSP-CL	AB020693 (SEQ ID NO: 310)

CPS No.	Corresponding Gene	Sequences Useful for Making Probe/Primers for Detecting the Corresponding Gene
281	NRG1	L41827 (SEQ ID NO: 311)
282	RAB31	U59877 (SEQ ID NO: 312)
283	MEF2D	L16794 (SEQ ID NO: 313)
284	UNK_AF038187	AF038187 (SEQ ID NO: 314)
285	CXCR4	L06797 (SEQ ID NO: 317)
286	M9	AB019392 (SEQ ID NO: 318)
287	FAU	X65923 (SEQ ID NO: 319)
288	RPS6	X67309 (SEQ ID NO: 320); and SEQ ID NO: 330
289	BAG5	AB020680 (SEQ ID NO: 321)
290	UNK_AL022721	the complement of SEQ ID NO: 322 (AL022721); and SEQ ID NO: 329
291	DKZP586E0820	AL050147 (SEQ ID NO: 323)
292	NONO	U02493 (SEQ ID NO: 324)
293	UNK_AI743507	the complement of SEQ ID NO: 325 (AI743507); and SEQ ID NO: 331
294	MAPKAPK5	AF032437 (SEQ ID NO: 326)
295	UNK_U79297	U79297 (SEQ ID NO: 327)

[0077] CPS 1 corresponds to TLR2 which encodes toll-like receptor 2. TLR2 has LocusID: 7097, and is located on chromosome 4 with reported cytogenetic location 4q32. The protein encoded by TLR2 gene is a member of the Toll-like receptor (TLR) family which is believed to play a fundamental role in pathogen recognition and activation of innate immunity. TLRs are highly conserved from *Drosophila* to humans and share structural and functional similarities. They recognize pathogen-associated molecular patterns (PAMPs) that are expressed on infectious agents, and mediate the production of cytokines necessary for the development of effective immunity. The various TLRs exhibit different patterns of expression. TLR2 is reported to be expressed abundantly in peripheral blood leukocytes, and to mediate host response to Gram-positive bacteria and yeast via stimulation of NF-kappaB. TLR2 may also mediate the signal for apoptosis.

[0078] CPS 2 corresponds to SLC1A4 which encodes solute carrier family 1 (glutamate/neutral amino acid transporter), member 4. SLC1A4 has LocusID: 6509, and is localized on chromosome 2 with reported cytogenetic location 2p15-p13. The gene product is a sodium-dependent neutral amino acid transporter, and has independent chloride channel activity. It may function to equilibrate pools of neutral amino acids.

[0079] CPS 3 corresponds to LGALS3 which encodes lectin, galactoside-binding, soluble, 3 (galectin 3). LGALS3 has LocusID: 3958, and is localized on chromosome 14 with reported cytogenetic location 14q21-q22. LGALS3 may be involved in cell growth regulation.

[0080] CPS 4 corresponds to DUSP6 which encodes dual specificity phosphatase 6. DUSP6 has LocusID: 1848, and is localized on chromosome 12 with reported cytogenetic location 12q22-q23.

[0081] The protein encoded by DUSP6 gene is a member of the dual specificity protein phosphatase subfamily. These phosphatases may inactivate their target kinases by dephosphorylating both the phosphoserine/threonine and phosphotyrosine residues. They may negatively regulate members of the mitogen-activated protein (MAP) kinase superfamily (MAPK/ERK, SAPK/JNK, p38), which are associated with cellular proliferation and differentiation. Different members of the family of dual specificity phosphatases show distinct substrate specificities for various MAP kinases, different tissue distribution and subcellular localization, and different modes of inducibility of their expression by extracellular stimuli. It is reported that DUSP6 gene product inactivates ERK2, is expressed in a variety of tissues with high levels of expression in heart and pancreas, and is localized in the cytoplasm. Dual specificity protein phosphatase 6 may selectively dephosphorylate and inactivate MAP kinase.

[0082] CPS 5 corresponds to KHSRP which encodes KH-type splicing regulatory protein (FUSE binding protein 2). KHSRP has LocusID: 8570, and is localized on chromosome 19 with reported cytogenetic location 19p13.3. It is reported that KHSRP gene product is a component of a multiprotein complex and may be involved in the splicing of the N1 exon of SRC. The genomic sequence (nucleotides 544983 to 544793 of chromosome 19) that aligns to CPS 5 is located 3' to the polypeptide-coding sequence of KHSRP. This genomic sequence is also located 3' to the polypeptide-coding sequence of LOC125980. LOC125980 encodes a protein similar to complement C3 precursor (human). It has reported cytogenetic location 19p13.3.

[0083] Nucleotides 1-501 of SEQ ID NO: 241 (AA628946) have about 99% sequence identity to KHSRP. Consequently, SEQ ID NO: 241 can be used to design probes for detecting the expression profile of KHSRP. Nucleotides 1-286 of SEQ ID NO: 241 also show about 89-93% sequence identity to a genomic sequence near the polypeptide-coding sequence of putative gene LOC138679. LOC138679 encodes a protein similar to KH-type splicing regulatory protein (FUSE binding protein 2) and KH-type splicing regulatory protein (FUSE-binding protein 2). LOC138679 is located on chromosome 9 with reported cytogenetic location 9p21.1.

[0084] CPS 6 corresponds to T54 which encodes T54 protein. T54 has LocusID: 27238, and is localized on chromosome X with reported cytogenetic location Xp11.23. T54 protein has a region of low similarity to *S. cerevisiae* Spp2p.

[0085] CPS 7 corresponds to RAB13, member RAS oncogene family. RAB13 has LocusID: 5872, and is localized on chromosome 1 with reported cytogenetic location 1q21.2. RAB13 gene product is known as GTP-binding protein 13, and may be involved in vesicle transport. It is a member of the RAB family of small GTPases. Nucleotides 106-1212 of SEQ ID NO: 7 (X75593) also align to a genomic sequence localized on chromosome 12 with reported cytogenetic location 12q13.

[0086] CPS 8 corresponds to a genomic sequence (DGCR5) at DiGeorge syndrome critical region 5 on chromosome 22. The corresponding genomic sequence is located 3' to the coding sequence of putative gene LOC128966 (similar to carbonic anhydrase 15). LOC128966 has LocusID: 9993, and is localized at cytogenetic location 22q11.1.

[0087] CPS 8 also shows about 97% sequence identity to a genomic sequence near the putative gene LOC91208 on chromosome 22. LOC91208 has reported cytogenetic location 22q11.21.

[0088] Blast search of X91348 (SEQ ID NO: 8) shows a corresponding genomic sequence which is localized on chromosome 22. The genomic sequence includes putative gene LOC200301 (similar to KIAA1647 protein) and DiGeorge syndrome gene A (DGS-A). DGS-A has LocusID: 25787. Deletions of the region near 22q11.2 have been associated with a wide range of developmental defects (notably DiGeorge syndrome, velocardiofacial syndrome, conotruncal anomaly face syndrome and isolated conotruncal cardiac defects) classified under the acronym CATCH 22.

[0089] In addition, fragments of nucleotides 132 to 699 of X91348 have 91% sequence identity to CELSR1 which encodes cadherin, EGF LAG seven-pass G-type

receptor 1 (flamingo homolog, *Drosophila*). CELSR1 has LocusID: 9620, and is also localized on chromosome 22.

[0090] CPS 9 corresponds to ENIGMA which encodes enigma (LIM domain protein). ENIGMA has LocusID: 9260, and is localized on chromosome 5 with reported cytogenetic location 5q35.3. The protein encoded by this gene is representative of a family of proteins composed of conserved PDZ and LIM domains. LIM domains are proposed to function in protein-protein recognition in a variety of contexts including gene transcription and development and in cytoskeletal interaction. The LIM domains of ENIGMA gene product may bind to protein kinases, whereas the PDZ domain may bind to actin filaments. The gene product may be involved in the assembly of an actin filament-associated complex essential for transmission of *ret/ptc2* mitogenic signaling. The biological function of ENIGMA gene product is proposed to be that of an adapter, with the PDZ domain localizing the LIM-binding proteins to actin filaments of both skeletal muscle and nonmuscle tissues. It is also reported that ENIGMA gene product can bind to the insulin receptor (INSR).

[0091] CPS 9 also has about 99% sequence identity to LOC220783 which encodes a protein similar to enigma (LIM domain protein). LOC220783 is localized on chromosome 5 with reported cytogenetic location 5q35.3.

[0092] CPS 10 corresponds to ETS2 which encodes v-ets erythroblastosis virus E26 oncogene homolog 2 (avian). ETS2 has LocusID: 2114, and is localized on chromosome 21 with reported cytogenetic location 21q22.2. ETS2 gene product is believed to be a transcription factor, and may have a role in some skeletal abnormalities in Downs syndrome.

[0093] CPS 11 corresponds to PIP5K1C which encodes phosphatidylinositol-4-phosphate 5-kinase, type I, gamma. PIP5K1C has LocusID: 23396, and is localized on chromosome 19 with reported cytogenetic location 19p13.3.

[0094] CPS 12 corresponds to TCFL1 which encodes transcription factor-like 1. The gene has LocusID: 6944, and is localized on chromosome 1 with reported cytogenetic location 1q21. The coding sequence of putative gene LOC148320 is located within TCFL1. LOC148320 also aligns with CPS 12.

[0095] CPS 13 can be derived from *Homo sapiens* mRNA for unknown liver orphan. The hypothetical gene(s) which corresponds to CPS 13 and produces the RNA

transcripts capable of hybridizing under stringent conditions to CPS 13 is herein referred to as UNK-AF055000.

[0096] CPS 14 corresponds to IL1RAP which encodes interleukin 1 receptor accessory protein. The gene has LocusID: 3556, and is localized on chromosome 3 with reported cytogenetic location 3q28. The gene product is a co-receptor for IL-1RI (IL1R1).

[0097] CPS 15 corresponds to REL which encodes v-rel reticuloendotheliosis viral oncogene homolog (avian). The gene has LocusID: 5966, and is localized on chromosome 2 at reported cytogenetic location 2p13-p12. The gene product is considered to be a transcription factor.

[0098] CPS 16 corresponds to ITGA7 which encodes integrin, alpha 7. The gene has LocusID: 3679, and is localized on chromosome 12 with reported cytogenetic location 12q13.

[0099] ITGA7 encodes integrin alpha chain 7. Integrins are heterodimeric integral membrane proteins composed of an alpha chain and a beta chain. Alpha chain 7 undergoes post-translational cleavage within the extracellular domain to yield disulfide-linked light and heavy chains that join with beta 1 to form an integrin that binds to the extracellular matrix protein laminin-1. Alpha 7 beta 1 is a major integrin complex expressed in differentiated muscle cells. Splice variants of alpha 7 that differ in both the extracellular and cytoplasmic domains exist in the mouse. However, to date only a single human transcript type has been isolated. It contains extracellular and cytoplasmic domains corresponding to the mouse X2 and B variants, respectively. A unique extracellular splice variant has been identified in human, although it may represent a minor species and its biological significance is unclear. Alpha 7 subunit of integrin is a laminin receptor.

[0100] Affymetrix annotation suggests that CPS 17 corresponds to PPARD. Blast search against the Entrez human genome database shows that CPS 17 also aligns to LOC221486 with over 98% sequence identity. LOC221486 encodes a protein similar to peroxisome proliferator activated receptor beta (PPAR-beta) (PPAR-delta) (Nuclear hormone receptor 1) (NUC1) (NUC1). The gene is localized on chromosome 6 with reported cytogenetic location 6p21.1.

[0101] CPS 18 corresponds to IL1RN which encodes interleukin 1 receptor antagonist. The gene has LocusID: 3557, and is localized on chromosome 2 with reported cytogenetic location 2q14.2. The gene product can bind to and inhibit the IL-1 receptor. The gene product is a member of the interleukin-1 (IL-1) family.

[0102] CPS 19 corresponds to LILRB3 which encodes leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3. The gene has LocusID: 11025, and is localized at chromosome 19 with reported cytogenetic location 19q13.4. The gene product may play a role in regulation of immune responses. It is a member of the immunoglobulin superfamily.

[0103] CPS 19 also shows about 99% sequence identity to LOC163021. LOC163021 encodes a protein similar to immunoglobulin-like transcript 5. The gene is localized on chromosome 19 with reported cytogenetic location 19q13.42.

[0104] CPS 20 corresponds to FOXO3A which encodes forkhead box O3A. The gene has LocusID: 2309, and is localized at chromosome 6 with reported cytogenetic location 6q21. The gene product belongs to the forkhead family of transcription factors which are characterized by a distinct forkhead domain. This gene may function as a trigger for apoptosis through expression of genes necessary for cell death. Translocation of this gene with the MLL gene may be associated with secondary acute leukemia.

[0105] Nucleotides 1-3183 of SEQ ID NO: 245 (AF032886) share at least 99% sequence identity to FOXO3A. Consequently, SEQ ID NO: 245 can be used to design probes for detecting the expression of FOXO3A. Nucleotides 672 to 3182 of SEQ ID NO: 245 also have 98% sequence identity to LOC147167. LOC147167 is similar to bA653O20.1 (forkhead box O3A (forkhead Drosophila homolog like 1, FKHRL1)). LOC147167 is localized on chromosome 17 with reported cytogenetic location 17p11.1.

[0106] CPS 21 corresponds to ANXA5 which encodes annexin A5. The gene has LocusID: 308, and is localized on chromosome 4 with reported cytogenetic location 4q28-q32. The gene product belongs to the annexin family of calcium-dependent phospholipid binding proteins, some of which have been implicated in membrane-related events along exocytotic and endocytotic pathways. The gene product is a phospholipase A2 and protein kinase C inhibitory protein with calcium channel activity and a potential role in cellular signal transduction, inflammation, growth and differentiation. The gene product has also been described as placental anticoagulant protein I, vascular anticoagulant-alpha, endonexin II, lipocortin V, placental protein 4 and anchorin CII. The gene contains at least 13 exons, and encodes at least one transcript of approximately 1.6 kb and at least one protein product with a molecular weight of about 35 kDa.

[0107] CPS 22 corresponds to SLC17A7 which encodes solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7. The gene has LocusID:

57030, and is localized on chromosome 19 with reported cytogenetic location 19q13. The protein encoded by this gene is highly similar to brain specific sodium-dependent inorganic phosphate cotransporter [R.norvegicus]. The protein is a vesicle-bound, sodium-dependent phosphate transporter. It may be associated with the membranes of synaptic vesicles and function in glutamate transport. The protein shares 82% identity with the differentiation-associated Na-dependent inorganic phosphate cotransporter.

[0108] CPS 23 corresponds to LOC51172 (APAA) which encodes N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase. The gene has LocusID: 51172, and is localized on chromosome 16 with reported cytogenetic location 16p13.13. N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase (phosphodiester alpha-GlcNAcase) catalyzes the second step in the synthesis of mannose 6-phosphate, and may be involved in forming the mannose 6-phosphate recognition signal on lysosomal enzymes.

[0109] CPS 24 corresponds to MPP1 which encodes membrane protein, palmitoylated 1 (55kD). The gene has LocusID: 4354, and is localized on chromosome X with reported cytogenetic location Xq28. Palmitoylated membrane protein 1 is the prototype of a family of membrane-associated proteins termed MAGUKs (membrane-associated guanylate kinase homologs). MAGUKs interact with the cytoskeleton and regulate cell proliferation, signaling pathways, and intracellular junctions. Palmitoylated membrane protein 1 contains a conserved sequence, called the SH3 (src homology 3) motif, which is found in several other proteins that associate with the cytoskeleton and is suspected to play important roles in signal transduction. Palmitoylated membrane protein 1 is similar to Drosophila dlg (a tumor suppressor) and guanylate kinases.

[0110] CPS 25 corresponds to TPM1 which encodes tropomyosin 1 (alpha). The gene has LocusID: 7168, and is localized on chromosome 15 with reported cytogenetic location 15q22.1. Alpha-tropomyosin 1 binds to actin and troponin, and is a member of a family of actin-binding and troponin-binding proteins.

[0111] CPS 26 corresponds to UNK_M62896 which shows about 99% sequence identity with the non-protein coding strand of TRIM2 gene. TRIM2 encodes tripartite motif-containing 2, and has LocusID: 23321 with reported cytogenetic location 4q31.23.

[0112] CPS 26 shows about 86-90% sequence similarity to LOC221025 and ANXA2P2. LOC221025 is a hypothetical gene supported by M62895. LOC221025 is localized on chromosome 10. ANXA2P2 is localized on chromosome 9, and encodes

annexin A2 pseudogene 2. In addition, CPS 26 has 91-93% sequence identity with two exons of ANXA2. ANXA2 encodes annexin A2, and has LocusID: 302 with reported cytogenetic location 15q21-q22.

[0113] CPS 27 corresponds to CSF2 which encodes colony stimulating factor 2 (granulocyte-macrophage). The gene has LocusID: 1437, and is localized on chromosome 5 with reported cytogenetic location 5q31.1. Granulocyte-macrophage colony stimulating factor 2 regulates hematopoietic cell differentiation, gene expression, and growth.

[0114] CPS 28 corresponds to LHFPL2 which encodes lipoma HMGIC fusion partner-like 2. The gene has LocusID: 10184, and is localized on chromosome 5 with reported cytogenetic location 5q13.3. Part of CPS 28 has about 90% sequence identity to LOC220397. LOC220397 encodes high mobility group protein 4 (HMG-4) (High mobility group protein 2a) (HMG-2a), and is localized on chromosome 11 with reported cytogenetic location 11q14.2.

[0115] CPS 29 corresponds to PARVB which encodes parvin, beta. The gene has LocusID: 29780, and is localized on chromosome 22 with reported cytogenetic location 22q13.2-q13.33. The gene product is also known as CGI-56 protein.

[0116] CPS 30 corresponds to MUC1 which encodes mucin 1, transmembrane. The gene has LocusID: 4582, and is localized on chromosome 1 with reported cytogenetic location 1q21. MUC1 gene product is a cell surface transmembrane glycoprotein. Alterations in glycosylation have been observed in epithelial cancer cells. MUC1 gene contains at least seven exons, and several alternatively spliced variants have been reported.

[0117] CPS 30 also has at least 99% sequence identity to LOC245755, which is a hypothetical gene supported by NM_002456 and X52228. LOC245755 is localized within MUC1.

[0118] CPS 31 corresponds to MARCO which encodes macrophage receptor with collagenous structure. The gene has LocusID: 8685, and is localized on chromosome 2 with reported cytogenetic location 2q12-q13. The gene protein has a collagenous structure that contains a bacteria-binding region.

[0119] CPS 32 corresponds to DRD2 which encodes dopamine receptor D2. The gene has LocusID: 1813, and is localized on chromosome 11 with reported cytogenetic location 11q23. This gene encodes the D2 subtype of the dopamine receptor. This G-protein coupled receptor can increase potassium channel activity, and inhibit adenylyl cyclase, calcium flux and phospholipid turnover. A missense mutation in this gene causes

myoclonus dystonia. Other mutations have been associated with schizophrenia. Alternative splicing of this gene results in two transcript variants encoding different isoforms. A third variant has been described, but it has not been determined whether this form is normal or due to aberrant splicing.

[0120] CPS 33 corresponds to PPY which encodes pancreatic polypeptide. The gene has LocusID: 5539, and is localized on chromosome 17 with reported cytogenetic location 17q21. The gene product is a precursor of the pancreatic polypeptide and pancreatic icosapeptide. Mature pancreatic peptide can inhibit pancreatic exocrine function.

[0121] CPS 34 corresponds to AQP9 which encodes aquaporin 9. The gene has LocusID: 366, and is localized on chromosome 15 with reported cytogenetic location 15q22.1-22.2. The aquaporins/major intrinsic protein are a family of water-selective membrane channels. Aquaporin 9 has greater sequence similarity with AQP3 and AQP7, and they may be a subfamily. Aquaporin 9 allows passage of a wide variety of noncharged solutes. Aquaporin 9 stimulates urea transport and osmotic water permeability. There are contradicting reports about its role in providing glycerol permeability. Aquaporin 9 may also have some role in specialized leukocyte functions such as immunological response and bactericidal activity. Aquaporin 9 is expressed in leukocytes

[0122] CPS 35 corresponds to APS which encodes adaptor protein with pleckstrin homology and src homology 2 domains. The gene has LocusID: 10603, and is localized on chromosome 7 with reported cytogenetic location 7q22. The APS protein, expressed in B lymphocytes, contains pleckstrin homology and src homology 2 (SH2) domains. In Burkitt lymphoma cell lines, it is tyrosine phosphorylated in response to B cell receptor stimulation. Because it binds Shc independent of stimulation and Grb2 after stimulation, it appears to play a role in signal transduction from the receptor to Shc/Grb2. It may link activated tyrosine kinases to signaling pathways.

[0123] CPS 36 corresponds to ALAS2 which encodes aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia). The gene has LocusID: 212, and is localized on chromosome X with reported cytogenetic location Xp11.21. The ALAS2 gene product catalyzes the first step in the heme biosynthetic pathway. A second delta-aminolevulinate synthase gene (ALAS1) is located on chromosome 3 and is expressed in various tissues. A defective ALAS2 gene may cause X-linked pyridoxine-responsive sideroblastic anemia (Hypochromic Anemia). The gene product is also known as erythroid-specific delta-aminolevulinate synthase.

[0124] CPS 36 has about 99% sequence identity to LOC203568. LOC203568 encodes a protein similar to 5-aminolevulinic acid synthase, erythroid-specific, mitochondrial precursor (Delta-aminolevulinate synthase) (Delta-ALA synthetase) (ALAS-E). The gene is located on chromosome X with reported cytogenetic location Xp11.22.

[0125] CPS 37 corresponds to CTSL which encodes cathepsin L. The gene has LocusID: 1514, and is located on chromosome 9 with reported cytogenetic location 9q21-q22. The gene product is a lysosomal cysteine (thiol) protease that can cleave collagen and elastin.

[0126] CPS 37 has about 80-90% sequence identity to certain other genes. These genes include LOC118945, LOC119215 and LOC219343. LOC118945 is similar to Cathepsin L precursor (Major excreted protein) (MEP). It is located on chromosome 10 with reported cytogenetic location 10q23.32. LOC119215 is also similar to Cathepsin L precursor (Major excreted protein) (MEP). It has reported cytogenetic location 10q21.1. LOC219343 has reported cytogenetic location 10q23.2.

[0127] CPS 38 corresponds to DKFZP586E1621 which encodes Ras-induced senescence 1. The gene has LocusID: 25907, and is located on chromosome 3 with reported cytogenetic location 3p21.3. The gene is also known as RIS1.

[0128] CPS 39 corresponds to PRO2389 which encodes a hypothetical protein. The gene has LocusID: 80344, and is localized on chromosome 14 with reported cytogenetic location 14q11.2. The gene product is weakly similar to a 38kDa splicing factor [H.sapiens].

[0129] CPS 40 corresponds to BLVRB which encodes biliverdin reductase B (flavin reductase (NADPH)). The gene has LocusID: 645, and is located on chromosome 19 with reported cytogenetic location 19q13.1-q13.2.

[0130] CPS 41 corresponds to GNA13 which encodes guanine nucleotide binding protein (G protein), alpha 13. The gene has LocusID: 10672, and is located on chromosome 17 with reported cytogenetic location 17q22-q24. The gene product is a component of heterotrimeric G-protein complexes.

[0131] CPS 41 shows about 75-80% sequence similarity to a genomic sequence near LOC130117. LOC130117 is similar to zinc finger protein 10 (KOX 1), and located on chromosome 2 with reported cytogenetic location 2p11.2.

[0132] CPS 42 corresponds to MAP2K3 which encodes mitogen-activated protein kinase kinase 3. The gene has LocusID: 5606, and is located on chromosome 17 with

reported cytogenetic location 17q11.2. The protein encoded by this gene is a dual specificity protein kinase that belongs to the MAP kinase kinase family. This kinase can be activated by mitogenic and environmental stress, and may participate in the MAP kinase-mediated signaling cascade. It can phosphorylate and thus activate MAPK14/p38-MAPK. This kinase can also be activated by insulin, and may be necessary for the expression of glucose transporter. Expression of RAS oncogene is found to result in the accumulation of the active form of this kinase, which thus leads to the constitutive activation of MAPK14, and confers oncogenic transformation of primary cells. The inhibition of this kinase is involved in the pathogenesis of Yersina pseudotuberculosis. Three alternatively spliced transcript variants of this gene encoding distinct isoforms have been reported.

[0133] CPS 42 has about 96-98% sequence identity to LOC146732. LOC146732 is similar to MAP kinase kinase 3b, and has reported cytogenetic location 17p13.1.

[0134] CPS 43 corresponds to BASP1 which encodes brain abundant, membrane attached signal protein 1. The gene has LocusID: 10409, and is located on chromosome 5 with reported cytogenetic location 5p15.1-p14. Nucleotides 433 to 554 of AA135683 also has 91% sequence identity to putative gene LOC222467 which is located on chromosome 13 with reported cytogenetic location 13q12.11.

[0135] CPS 44 corresponds to BNIP3L which encodes BCL2/adenovirus E1B 19kD interacting protein 3-like. The gene has LocusID: 665, and is located on chromosome 8 with reported cytogenetic location 8p21. This gene is a member of the BCL2/adenovirus E1B 19 kd-interacting protein (BNIP) family. BNIP3L gene product can interact with the E1B 19 kDa protein which is responsible for the protection of virally-induced cell death. The gene product is a functional homolog of BNIP3, a proapoptotic protein. The gene product may function simultaneously with BNIP3 and play a role in tumor suppression. The gene product can also bind cellular Bcl2 or Bcl2L1, and may promote apoptosis.

[0136] CPS 45 corresponds to DBP which encodes D site of albumin promoter (albumin D-box) binding protein. The gene has LocusID: 1628, and is located on chromosome 19 with reported cytogenetic location 19q13.3. The gene product may function as a transcription factor and play a role in the diurnal regulation of liver-specific genes. It is a member of the PAR (proline and acidic amino acid-rich) b/ZIP family.

[0137] CPS 46 corresponds to BACH (hBACH) which encodes brain acyl-CoA hydrolase. The gene has LocusID: 11332, and is located on chromosome 1 with reported cytogenetic location 1p36.31-p36.11. The gene product is a member of the acyl coenzyme

family. It can hydrolyze the CoA thioester of palmitoyl-CoA and other long-chain fatty acids. The gene product is also known as cytosolic acyl coenzyme A thioester hydrolase.

[0138] Nucleotides 76-1101 of SEQ ID NO: 46 (U91316) have about 89% sequence identity to LOC132927 which encodes a protein similar to cytosolic acyl coenzyme A thioester hydrolase (Long chain acyl-CoA thioester hydrolase) (CTE-II) (Brain acyl-CoA hydrolase) (BACH). LOC132927 is located on chromosome 4 with reported cytogenetic location 4p14.

[0139] CPS 47 corresponds to DGAT1 which encodes diacylglycerol O-acyltransferase homolog 1 (mouse). The gene has LocusID: 8694, and is located on chromosome 8 with reported cytogenetic location 8qter. The enzyme encoded by this gene utilizes diacylglycerol and fatty acyl CoA as substrates in order to catalyze the final stage of triacylglycerol synthesis. It is also involved in cellular as well as physiological metabolic processes.

[0140] CPS 48 corresponds to GUK1 which encodes guanylate kinase 1. The gene has LocusID: 2987, and is located on chromosome 1 with reported cytogenetic location 1q32-q41. The gene product can convert GMP to GTP as part of the cGMP cycle.

[0141] CPS 49 corresponds to IL10RB which encodes interleukin 10 receptor, beta. The gene has LocusID: 3588, and is located on chromosome 21 with reported cytogenetic location 21q22.11. Interleukin 10 receptor beta subunit transduces a signal upon binding of interleukin-10 (IL10). It is a class II member of the cytokine receptor family (CRF2).

[0142] The chromosomal region that aligns to CPS 49 is also located 3' to the polypeptide-coding sequence of IFNAR2. IFNAR2 encodes interferon (alpha, beta and omega) receptor 2. The gene has LocusID: 3455, and is located on chromosome 21 with reported cytogenetic location 21q22.11.

[0143] CPS 50 corresponds to ENPP2 (PDNP2) which encodes ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin). The gene has LocusID: 5168, and is located on chromosome 8 with reported cytogenetic location 8q24.1. Autotaxin is a potent tumor cell motility-stimulating protein. The gene product is also known as phosphodiesterase I/nucleotide pyrophosphatase 2 (autotaxin).

[0144] Nucleotides 375-452, 1241-1277, 1576-1761 and 1399-1488 of SEQ ID NO: 50 (D45421) also have 97-100% sequence identity to a genomic sequence near LOC206890 on chromosome 8. LOC206890 is similar to cytochrome c (somatic) and has reported cytogenetic location 8q12.3.

[0145] CPS 51 corresponds to SLC5A6 which encodes solute carrier family 5 (sodium-dependent vitamin transporter), member 6. The gene has LocusID: 8884, and is located on chromosome 2 with reported cytogenetic location 2p23. The gene product functions in the transplacental transfer of pantothenate biotin and lipoate. Nucleotides 962 to 1314 of SEQ ID NO: 51 (AL096737) has about 90% identity to TCF23 (LocusID: 150921) which encodes transcription factor 23 and is located on chromosome 2 with reported cytogenetic location 2p23.3.

[0146] CPS 52 corresponds to GPR3 which encodes G protein-coupled receptor 3. The gene has LocusID: 2827, and is located on chromosome 1 with reported cytogenetic location 1p36.1-p35. The gene product can activate adenylate cyclase in cell lines, and is a member of the G protein-coupled receptor family.

[0147] CPS 53 corresponds to SOD2 which encodes superoxide dismutase 2, mitochondrial. The gene has LocusID: 6648, and is located on chromosome 6 with reported cytogenetic location 6q25.3. The gene product is an intramitochondrial free radical scavenging enzyme, and has strong similarity to murine Sod2.

[0148] CPS 54 corresponds to TREX1 which encodes three prime repair exonuclease 1. The gene has LocusID: 11277, and is located on chromosome 3 with reported cytogenetic location 3p21.3-p21.2. This gene uses at least two different open reading frames. The upstream ORF encodes proteins which interact with the ataxia telangiectasia and Rad3 related protein, a checkpoint kinase. The proteins encoded by this upstream ORF localize to intranuclear foci following DNA damage and may be important components of the DNA damage checkpoint. The downstream ORF encodes proteins with 3' exonuclease activity. Other enzymes with this activity are involved in DNA replication, repair, and recombination. Similarity to an E. coli protein suggests that the enzymes encoded by this ORF may be a subunit of DNA polymerase III, which does not have intrinsic exonuclease activity. Both ORFs are subject to alternative splicing, resulting in at least six transcript variants.

[0149] CPS 54 also has about 99% sequence identity to at least parts of LOC200884 and LOC152456. Both genes are located within TREX1. LOC200884 encodes protein(s) similar to three prime repair exonuclease 1 (isoform b), 3 repair exonuclease 1, deoxyribonuclease III (dnaQ/mutD (E. coli)-like), and ATR interacting protein. LOC200884 has reported cytogenetic location 3p21.31. LOC152456 encodes protein(s) similar to three prime repair exonuclease 1 (isoform b), 3 repair exonuclease 1,

deoxyribonuclease III (dnaQ/mutD (E. coli)-like), and ATR interacting protein. It has reported cytogenetic location 3p21.31.

[0150] CPS 55 corresponds to WNT6 which encodes wingless-type MMTV integration site family, member 6. The gene has LocusID: 7475, and is located on chromosome 2 with reported cytogenetic location 2q35. The WNT gene family consists of structurally related genes which encode secreted signaling proteins. These proteins have been implicated in oncogenesis and in several developmental processes, including regulation of cell fate and patterning during embryogenesis. This gene is a member of the WNT gene family. It is overexpressed in a cervical cancer cell line and strongly coexpressed with another family member, WNT10A, in a colorectal cancer cell line. The gene overexpression may play key roles in carcinogenesis. This gene and the WNT10A gene are clustered in the chromosome 2q35 region. The protein encoded by this gene is 97% identical to the mouse Wnt6 protein at the amino acid level.

[0151] CPS 56 corresponds to PIP5K2A which encodes phosphatidylinositol-4-phosphate 5-kinase, type II, alpha. The gene has LocusID: 5305, and is located on chromosome 10 with reported cytogenetic location 10p11.23. Phosphatidylinositol-4,5-bisphosphate, the precursor to second messengers of the phosphoinositide signal transduction pathways, is thought to be involved in the regulation of secretion, cell proliferation, differentiation, and motility. The protein encoded by this gene is one of a family of enzymes capable of catalyzing the phosphorylation of phosphatidylinositol-4-phosphate on the fifth hydroxyl of the myo-inositol ring to form phosphatidylinositol-4,5-bisphosphate. The gene product exhibits kinase activity. This gene is a member of the phosphatidylinositol-4-phosphate 5-kinase family. The gene product is also known as 1-phosphatidylinositol-4-phosphate-5-kinase isoform C.

[0152] CPS 57 corresponds to FABP5 which encodes fatty acid binding protein 5 (psoriasis-associated). FABP5 gene has LocusID: 2171, and is located on chromosome 8 with reported cytogenetic location 8q21.13. The gene encodes the fatty acid binding protein found in epidermal cells, and was identified as being upregulated in psoriasis tissue. Fatty acid binding proteins are a family of small, highly conserved, cytoplasmic proteins that bind long-chain fatty acids and other hydrophobic ligands. It is thought that fatty acid binding proteins are involved in fatty acid uptake, transport, and metabolism. FABP5 gene product binds to stearic acid and may have a role in keratinocyte differentiation.

[0153] CPS 57 also shows 100% sequence alignment with an intron sequence of STX3A which encodes syntaxin 3A. The gene has LocusID: 6809, and is located on chromosome 11 with reported cytogenetic location 11q12.3. Syntaxin 3A is involved in intracellular protein transport.

[0154] In addition, CPS 57 has about 95-97% sequence identity to LOC95551, LOC220113, LOC114948, LOC220832, and LOC150161. LOC95551 is similar to fatty acid-binding protein, epidermal (E-FABP) (psoriasis-associated fatty acid-binding protein homolog) (PA-FABP). LOC95551 is located on chromosome 13 with reported cytogenetic location 13q21.33. LOC220113 encodes fatty acid-binding protein, epidermal (E-FABP) (psoriasis-associated fatty acid-binding protein homolog) (PA-FABP). LOC220113 has reported cytogenetic location 13q14.13. LOC220113 is within an intron of ATP7B which encodes ATPase, Cu⁺⁺ transporting, beta polypeptide (Wilson disease), and has LocusID: 540.

[0155] LOC114948 encodes a protein similar to fatty acid-binding protein, epidermal (E-FABP) (psoriasis-associated fatty acid-binding protein homolog) (PA-FABP). It is located on chromosome 15 with reported cytogenetic location 15q25.3. LOC220832 also encodes a protein similar to fatty acid-binding protein, epidermal (E-FABP) (psoriasis-associated fatty acid-binding protein homolog) (PA-FABP). It has reported cytogenetic location 7q36.1. Similarly, LOC150161 encodes a protein similar to fatty acid-binding protein, epidermal (E-FABP) (psoriasis-associated fatty acid-binding protein homolog) (PA-FABP). It is located on chromosome 22 with reported cytogenetic location 22q11.1.

[0156] Furthermore, CPS 57 has about 89-93% sequence identity to BTBD1, LOC130962, LOC152940 and LOC204114. BTBD1 encodes BTB (POZ) domain containing 1. It has LocusID: 53339, and is located on chromosome 15 with reported cytogenetic location 15q24. The gene product contains a BTB/POZ domain, and may function as DNA or actin binding protein. LOC130962 encodes a protein similar to fatty acid-binding protein, epidermal (E-FABP) (psoriasis-associated fatty acid-binding protein homolog) (PA-FABP). The gene has reported cytogenetic location 2q23.3. Likewise, LOC152940 encodes a protein similar to unnamed protein product. It is located on chromosome 4 with reported cytogenetic location 4q31.3-q32.1. LOC204114 encodes a protein similar to fatty acid binding protein homolog. It has reported cytogenetic location 13q31.3.

[0157] CPS 58 corresponds to MMP9 which encodes matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase). The gene has LocusID: 4318, and is located on chromosome 20 with reported cytogenetic location 20q11.2-q13.1. Proteins of the matrix metalloproteinase (MMP) family are involved in the breakdown of extracellular matrix in normal physiological processes, such as embryonic development, reproduction, and tissue remodeling, as well as in disease processes, such as arthritis and metastasis. Most MMPs are secreted as inactive proproteins which are activated when cleaved by extracellular proteinases. The enzyme encoded by this gene can degrade type IV and V collagens. Studies in rhesus monkeys suggest that the enzyme is involved in IL-8-induced mobilization of hematopoietic progenitor cells from bone marrow, and murine studies suggest a role in tumor-associated tissue remodeling.

[0158] CPS 59 corresponds to ATP2B1 which encodes ATPase, Ca⁺⁺ transporting, plasma membrane 1. The gene has LocusID: 490, and is located on chromosome 12 with reported cytogenetic location 12q21-q23.

[0159] Nucleotides 2623 to 2814 of SEQ ID NO: 59 (J04027) have about 81% sequence identity to ATP2B4 which encodes ATPase, Ca⁺⁺ transporting, plasma membrane 4. ATP2B4 has LocusID: 493, and is located on chromosome 1. Nucleotides 4365-4398 of SEQ ID NO: 59 has 100% sequence identity to FLJ14075 which encodes hypothetical protein FLJ14075. FLJ14075 has LocusID: 79954, and is located on chromosome 2.

[0160] CPS 60 corresponds to NEUD4 which encodes neuro-d4 (rat) homolog. The gene has LocusID: 8193, and is located on chromosome 19 with reported cytogenetic location 19q13.13. The gene product contains at least a zinc finger DNA binding domain. Nucleotides 61-198 of U43843 has 86% sequence identity to CERD4 which encodes cer-d4 (mouse) homolog. CERD4 has LocusID: 8110, and is located on chromosome 14 with reported cytogenetic location 14q24.3-q31.1.

[0161] CPS 61 corresponds to CCR1 which encodes chemokine (C-C motif) receptor 1. The gene has LocusID: 1230, and is located on chromosome 3 with reported cytogenetic location 3p21. The gene products is a member of the beta chemokine receptor family, and is predicted to be a seven transmembrane protein similar to G protein-coupled receptors. The ligands of this receptor include macrophage inflammatory protein 1 alpha (MIP-1 alpha), monocyte chemoattractant protein 3 (MCP-3), and myeloid progenitor inhibitory factor-1 (MPIF-1). Signal transduction mediated by chemokines and their receptors is believed to be important for the recruitment of effector immune cells to the site

of inflammation. Knockout studies of the mouse homolog suggests the role of this gene in host protection from inflammatory response, and susceptibility to virus and parasite. This gene and other chemokine receptor genes, including CCR2, CCRL2, CCR3, CCR5 and CCXCR1, are found to form a gene cluster on chromosome 3p. The protein encoded by this gene can bind to chemokines of the CC subfamily and mediate intracellular calcium flux.

[0162] CPS 62 corresponds to C8FW which encodes a phosphoprotein regulated by mitogenic pathways. The protein is similar to protein kinases. The gene has LocusID: 10221, and is located on chromosome 8 with reported cytogenetic location 8q24.13.

[0163] CPS 63 corresponds to CLU which encodes clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J). The gene has LocusID: 1191, and is located on chromosome 8 with reported cytogenetic location 8p21-p12. Clusterin is a glycoprotein and can be found in high density lipoproteins and endocrine and neuronal granules. It may have a role in the terminal complement reaction.

[0164] CPS 64 corresponds to EREG which encodes epiregulin. The gene has LocusID: 2069, and is located on chromosome 4 with reported cytogenetic location 4q13.3. Epiregulin is a member of the epidermal growth factor family. Epiregulin can function as a ligand of EGFR (epidermal growth factor receptor), as well as a ligand of members of the ERBB (v-erb-b2 oncogene homolog) family of tyrosine-kinase receptors. Epiregulin may promote cell proliferation.

[0165] CPS 65 corresponds to PPAP2B which encodes phosphatidic acid phosphatase type 2B. The gene has LocusID: 8613, and is located on chromosome 1 with reported cytogenetic location 1pter-p22.1. The gene product is magnesium-independent phosphatidic acid phosphatase 2b. It can convert phosphatidic acid to diacylglycerol. It can also hydrolyze lysophosphatidate, ceramide-1-phosphate, and sphingosine-1-phosphate.

[0166] CPS 66 corresponds to TUBB which encodes tubulin, beta polypeptide. The gene has LocusID: 7280, and is located on chromosome 6 with reported cytogenetic location 6p21.3. Beta tubulin can polymerize to form microtubules. It is a member of a family of structural proteins.

[0167] Nucleotides 119-231 and 340-939 of SEQ ID NO: 66 (X79535) also have over 99% sequence identity to a genomic sequence between TUBB and LOC221753. LOC221753 is located on chromosome 6.

[0168] In addition, nucleotides 58-120 and 340-1397 of X79535 have about 98% sequence identity to LOC221753. LOC221753 has reported cytogenetic location 6p24.3.

[0169] Moreover, fragments of X79535 exhibit about 82-92% sequence identity to certain other genes. These genes include TUBB5, TUBB4, LOC139112, LOC157586, LOC203068, LOC92755 and GABRR2. TUBB5 encodes tubulin, beta, 5. It has LocusID: 10382, and is located on chromosome 19 with reported cytogenetic location 19p13.3. TUBB5 gene has nucleotides 637115 to 644163 of chromosome 19. Beta 5-tubulin can polymerize to form microtubules. TUBB4 encodes tubulin, beta, 4. It has LocusID: 10381, and is located on chromosome 16 with reported cytogenetic location 16q24.3. Beta 4-tubulin can also polymerize to form microtubules. LOC139112 encodes a protein similar to tubulin beta. The gene has reported cytogenetic location Xq25. LOC157586 and LOC203068 encode proteins similar to hypothetical protein DKFZp564N123.1 - human (fragment). Both genes have reported cytogenetic location 8p21.1. LOC92755 is a hypothetical gene, and has reported cytogenetic location 8p21.1. GABRR2 encodes gamma-aminobutyric acid (GABA) receptor, rho 2. It has LocusID: 2570 and reported cytogenetic location 6q13-q16.3. GABA is a major inhibitory neurotransmitter in the mammalian brain where it can act at GABA receptors, which are ligand-gated chloride channels. GABRR2 is a member of the rho subunit family.

[0170] CPS 67 corresponds to NUP214 which encodes nucleoporin 214kD (CAIN). The gene has LocusID: 8021, and is located on chromosome 9 with reported cytogenetic location 9q34.1. Nucleoporin 214kD is a protein localized to cytoplasmic aspect of the nuclear pore complex. It contains FXFG repeats.

[0171] Fragment of nucleotides 3712 to 5515 of D14689 (SEQ ID NO: 67) has 100% sequence identity to LOC158306. LOC158306 encodes a protein similar to nucleoporin 214kD (CAIN), and has reported cytogenetic location 9q34.2. LOC158306 is located within an exon of NUP214 gene.

[0172] CPS 68 corresponds to ALDH5A1 which encodes aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase). The gene has LocusID: 7915, and is located on chromosome 6 with reported cytogenetic location 6p22. CPS 68 aligns to nucleotides 32909278 to 32909817 of chromosome 6, and is located in the 3' untranslated region of ALDH5A1. Aldehyde dehydrogenase 5A1 (succinic semialdehyde dehydrogenase) involves 4-aminobutyric acid degradation.

[0173] Nucleotides 45212 to 44763 of SEQ ID NO: 68 (AL031230) have about 90% sequence identity to HSPCAL3 which encodes heat shock 90kD protein 1, alpha-like 3. HSPCAL3 gene has LocusID: 3324 and reported cytogenetic location 11p14.2-p14.1. In addition, nucleotides 11858 to 12096 of AL031230 show 86% sequence identity to a genomic sequence on chromosome 1.

[0174] CPS 69 corresponds to LOC64116. The gene has LocusID: 64116, and is located on chromosome 4 with reported cytogenetic location 4q22-q24. The gene is up-regulated by BCG-CWS.

[0175] CPS 70 corresponds to XK which encodes Kell blood group precursor (McLeod phenotype). The gene has LocusID: 7504, and is located on chromosome X with reported cytogenetic location Xp21.1. This locus controls the synthesis of the Kell blood group "recursor substance" Kx). Mutations in this gene have been associated with McLeod syndrome, an X-linked, recessive disorder characterized by abnormalities in the neuromuscular and hematopoietic systems. The encoded protein is a member of transporter family and has structural characteristics of prokaryotic and eukaryotic membrane transport proteins.

[0176] CPS 71 corresponds to KIAA0837 (FACL6) which encodes long fatty acyl-CoA synthetase 2 gene (fatty-acid-Coenzyme A ligase, long-chain 6). The gene has LocusID: 23305, and is located on chromosome 5 with reported cytogenetic location 5q31.

[0177] CPS 72 corresponds to GYPC which encodes glycophorin C (Gerbich blood group). The gene has LocusID: 2995, and is located on chromosome 2 with reported cytogenetic location 2q14-q21. Glycophorin C (GYPC) is an integral membrane glycoprotein. It is a minor species carried by human erythrocytes, but plays an important role in regulating the mechanical stability of red cells. A number of glycophorin C mutations have been described. The Gerbich and Yus phenotypes are due to deletion of exon 3 and 2, respectively. The Webb and Duch antigens, also known as glycophorin D, result from single point mutations of the glycophorin C gene. The glycophorin C protein has homology with glycophorins A and B.

[0178] CPS 73 corresponds to TFDP1 which encodes transcription factor Dp-1. The gene has LocusID: 7027, and is located on chromosome 13 with reported cytogenetic location 13q34. The gene product may heterodimerize with E2F to transactivate genes involved in cell cycle progression from G1 to S-phase. TFDP1, CUL4A, and CDC16 are

probable targets of an amplification mechanism and may be involved, together or separately, in development and/or progression of some hepatocellular carcinomas.

[0179] CPS 73, as well as nucleotides 9 to 1440 of L23959 (SEQ ID NO: 73), have about 95% sequence identity to LOC245788 on chromosome 8. LOC245788 is reported to encode transcription factor DP-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1) (DRTF1).

[0180] In addition, CPS 73 has about 87-90% sequence identity to LOC126611 and LOC51270. LOC126611 encodes a protein similar to transcription factor DP-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1) (DRTF1). It is located on chromosome 1 with reported cytogenetic location 1q31.3. LOC51270 encodes E2F-like protein which is similar to a region of human transcription factor Dp-1. The gene has LocusID: 51270, and is located on chromosome X with reported cytogenetic location Xq26.2.

[0181] Nucleotides 1001 to 1440 of SEQ ID NO: 73 (L23959) have about 87% sequence identity to CD36 which encodes CD36 antigen (collagen type I receptor, thrombospondin receptor). The gene has LocusID: 948, and is located on chromosome 7 with reported cytogenetic location 7q11.2. CD36 is a receptor for thrombospondin and collagen in platelets. It functions in cell adhesion. It has a role in platelet-collagen adhesion, and can bind to long chain fatty acids. The protein is strongly similar to rat FAT. Nucleotides 9 to 947 of SEQ ID NO: 73 have 95% sequence identity to LOC123471 which encodes a protein similar to transcription factor DP-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1) (DRTF1). LOC123471 has reported cytogenetic location 15q23.

[0182] CPS 74 corresponds to C20orf16 which encodes chromosome 20 open reading frame 16. The gene has LocusID: 54498, and is located on chromosome 20 with reported cytogenetic location 20p13. The protein is a member of the flavin containing amine oxidase family. It is weakly similar to monoamine MAOB (oxidase B).

[0183] CPS 75 corresponds to FCAR which encodes a receptor for Fc fragment of IgA. The gene has LocusID: 2204, and is located on chromosome 19 with reported cytogenetic location 19q13.2-q13.4. This gene is a member of the immunoglobulin gene superfamily and encodes a receptor for the Fc region of IgA. The receptor is a transmembrane glycoprotein present on the surface of myeloid lineage cells such as neutrophils, monocytes, macrophages, and eosinophils, where it may mediate immunologic responses to pathogens. It may interact with IgA-opsonized targets and trigger several immunologic defense processes, including phagocytosis, antibody-dependent cell-mediated

cytotoxicity, and stimulation of the release of inflammatory mediators. At least ten transcript variants encoding different isoforms have been described for this gene. The gene product is also known as Fc alpha R.

[0184] CPS 76 corresponds to ITGB3 which encodes integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61). The gene has LocusID: 3690, and is located on chromosome 17 with reported cytogenetic location 17q21.32. The ITGB3 protein product is the integrin beta chain beta 3. Integrins are integral cell-surface proteins composed of an alpha chain and a beta chain. A given chain may combine with multiple partners resulting in different integrins. Integrin beta 3 is found along with the alpha IIb chain in platelets. Integrins are known to participate in cell adhesion as well as cell-surface mediated signaling. This gene product may be involved in mediating platelet aggregation.

[0185] CPS 77 corresponds to MXI1 which encodes MAX interacting protein. The gene has LocusID: 4601, and is located on chromosome 10 with reported cytogenetic location 10q24-q25. Expression of the c-myc gene, which produces an oncogenic transcription factor, is tightly regulated in normal cells but is frequently deregulated in human cancers. The protein encoded by this gene is a transcriptional repressor thought to negatively regulate MYC function, and is therefore a potential tumor suppressor. The protein inhibits the transcriptional activity of MYC by competing for MAX, another basic helix-loop-helix protein that binds to MYC and is required for its function. Defects in this gene are frequently found in patients with prostate tumors. Two transcript variants encoding different isoforms have been identified for this gene.

[0186] Nucleotides 1 to 64 of SEQ ID NO: 77 (L07648) show 100% sequence identity to ARHA which encodes ras homolog gene family, member A. The gene has LocusID: 387, and is located on chromosome 3 with reported cytogenetic location 3p21.3. The gene product is a ras-related GTP binding protein of the rho subfamily, and may be involved in regulation of reorganization of the actin cytoskeleton.

[0187] CPS 78 corresponds to CSDA which encodes cold shock domain protein A. The gene has LocusID: 8531, and is located on chromosome 12 with reported cytogenetic location 12p13.1. The gene product is a member of a family of transcriptional regulators. It can bind and repress the promoter of the (GM-CSF) gene. The gene product contains a cold-shock domain.

[0188] CPS 78, as well as nucleotides 14 to 1568 of M24069 (SEQ ID NO: 78), show at least 94% sequence identity to LOC220558. LOC220558 also encodes cold shock

domain protein A or cold-shock domain protein A. It is located on chromosome 16 with reported cytogenetic location 16p11.1.

[0189] CPS 79 corresponds to OPTN (FIP2) which encodes optineurin. The gene has LocusID: 10133, and is located on chromosome 10 with reported cytogenetic location 10p12.33. The gene product is a component of a heterodimeric complex that inhibits cytolysis induced by tumor necrosis factor alpha. It contains leucine zippers. It is also known as tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains or Huntingtin interacting protein L.

[0190] CPS 80 corresponds to SELENBP1 which encodes selenium binding protein 1. The gene has LocusID: 8991, and is located on chromosome 1 with reported cytogenetic location 1q21-q22. This gene product belongs to the selenium-binding protein family. Selenium is a nutrient that exhibits potent anticarcinogenic properties, and deficiency of selenium may cause certain neurologic diseases. It has been proposed that the effects of selenium in preventing cancer and neurologic diseases may be mediated by selenium-binding proteins. The exact function of this gene is not known.

[0191] CPS 81 corresponds to PPP1R2 which encodes protein phosphatase 1, regulatory (inhibitor) subunit 2. The gene has LocusID: 5504, and is located on chromosome 3 with reported cytogenetic location 3q29. Inhibitory subunit 2 of protein phosphatase 1 may associate with the gamma isoform of protein phosphatase 1.

[0192] Nucleotides 25 to 556 of SEQ ID NO: 81 (U68111) also have 96% sequence identity to LOC153743. This gene encodes a protein similar to protein phosphatase 1, regulatory (inhibitor) subunit 2. The gene has reported cytogenetic location 5q33.2.

[0193] In addition, nucleotides 25 to 556 of U68111 have 85-90% sequence identity to certain other genes or genomic sequences. These genes or genomic sequences include PPP1R2P1, the region 3' to LOC160817, the non-coding region of LOC130957, the non-coding region of LOC220419, and certain regions in chromosomes 7 and 21. PPP1R2P1 encodes protein phosphatase 1, regulatory (inhibitor) subunit 2 pseudogene 1. PPP1R2P1 has LocusID: 5505, and is located on chromosome 6 with reported cytogenetic location 6p21.1. LOC160817 encodes a protein similar to protein phosphatase 1, regulatory (inhibitor) subunit 2, and has reported cytogenetic location 13q21.1. LOC130957 encodes a protein similar to protein phosphatase 1, regulatory (inhibitor) subunit 2, and is located at chromosome 2q12.1. LOC220419 is reported to encode protein phosphatase 1, regulatory (inhibitor) subunit 2, and is located at chromosome 13q14.11.

[0194] CPS 82 corresponds to HPGD which encodes hydroxyprostaglandin dehydrogenase 15-(NAD). The gene has LocusID: 3248, and is located on chromosome 4 with reported cytogenetic location 4q34-q35. The gene product can inactivate many prostaglandins by oxidation of their C-15 residues.

[0195] CPS 83 corresponds to SLC4A1 which encodes solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group). The gene has LocusID: 6521, and is located on chromosome 17 with reported cytogenetic location 17q21-q22. The genomic sequence aligning to CPS 83 is located 3' to the polypeptide-coding sequence of the gene. The gene is also known as CD233 gene. The gene product, also known as Band 3 anion exchanger, is part of the anion exchanger (AE) family. The gene product may function to maintain ion homeostasis by transporting chloride and bicarbonate ions.

[0196] SEQ ID NO: 259 (M27819) also aligns to SLC4A1 with over 98% sequence identity, and therefore, can be used as a probe for SLC4A1. Nucleotides 2206 to 2426 of SEQ ID NO: 259 also show about 76% sequence identity to SLC4A2. This gene encodes solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1). The gene has LocusID: 6522.

[0197] CPS 84 corresponds to IL17R which encodes interleukin 17 receptor. The gene has LocusID: 23765, and is located on chromosome 22 with reported cytogenetic location 22q11.1. The gene product is highly similar to murine Il17r, and may play a role in T cell activation and induction of IL-2 (IL2).

[0198] CPS 87 corresponds to CBFA2T3 which encodes core-binding factor, runt domain, alpha subunit 2; translocated to, 3. The gene has LocusID: 863, and is located on chromosome 16 with reported cytogenetic location 16q24. The gene product is a member of the MTG8 (ETO/CDR) protein family.

[0199] CPS 89 corresponds to an intron sequence of RAP1GA1. RAP1GA1 encodes GTPase activating protein 1 for rap1. RAP1GA1 gene has LocusID: 5909, and is located on chromosome 1 with reported cytogenetic location 1p36.1-p35. The gene product is also known as KIAA0474 gene product.

[0200] CPS 90 corresponds to BCL2L1 which encodes BCL2-like 1. The gene has LocusID: 598, and is located on chromosome 20 with reported cytogenetic location 20q11.1. The protein encoded by this gene belongs to the BCL-2 protein family. BCL-2 family members form hetero- or homodimers and act as anti- or pro-apoptotic regulators

that are involved in a wide variety of cellular activities. The proteins encoded by this gene are located at the outer mitochondrial membrane, and have been shown to regulate outer mitochondrial membrane channel (VDAC) opening. VDAC regulates mitochondrial membrane potential, and thus controls the production of reactive oxygen species and release of cytochrome C by mitochondria, both of which are the potent inducers of cell apoptosis. At least two alternatively spliced transcript variants, which encode distinct isoforms, have been reported. The longer isoform may act as an apoptotic inhibitor and the shorter form may act as an apoptotic activator.

[0201] CPS 91 corresponds to COPEB which encodes core promoter element binding protein. The gene has LocusID: 1316, and is located on chromosome 10 with reported cytogenetic location 10p15. This gene encodes a nuclear protein (core promoter element binding protein). This protein has three zinc fingers at the end of its C-terminal domain, a serine/threonine-rich central region and an acidic domain lying within the N-terminal region. The zinc fingers of this protein are believed to be responsible for the specific DNA binding with the guanine-rich core promoter elements. The central region might be involved in activation or posttranslational regulatory pathways, and the acidic N-terminal domain might play an important role in the process of transcriptional activation. This protein is expressed in several tissues, with the high levels in the placenta. It is a transcriptional activator, capable of activating transcription approximately 4-fold either on homologous or heterologous promoters. The DNA binding and transcriptional activity of this protein, in conjunction with its expression pattern, suggests that this protein may participate in the regulation and/or maintenance of the basal expression of pregnancy-specific glycoprotein gene and possibly other TATA box-less genes. The genomic sequence aligning to CPS 91 is located 3' to the polypeptide coding sequence of the gene.

[0202] CPS 92 corresponds to ADM which encodes adrenomedullin. The gene has LocusID: 133, and is located on chromosome 11 with reported cytogenetic location 11p15.4. Adrenomedullin, a hypotensive peptide found in human pheochromocytoma, consists of 52 amino acids, has one intramolecular disulfide bond, and shows a slight homology with the calcitonin gene-related peptide. It may function as a hormone in circulation control because it is found in blood in a considerable concentration. The precursor, called preproadrenomedullin, is 185 amino acids long. By RNA-blot analysis, human adrenomedullin mRNA was found to be highly expressed in several tissues. Genomic ADM DNA consists of at least 4 exons and 3 introns, with the 5-prime flanking

region containing TATA, CAAT, and GC boxes. There are also multiple binding sites for activator protein-2 and a cAMP-regulated enhancer element. The gene also encodes the precursor of adrenomedullin (AM) and the putative 20 amino acid peptide proAM-N20. The gene product may regulate blood pressure and heart rate.

[0203] CPS 93 corresponds to SPTB which encodes spectrin, beta, erythrocytic (includes spherocytosis, clinical type I). The gene has LocusID: 6710, and is located on chromosome 14 with reported cytogenetic location 14q23-q24.2. Beta spectrin (beta-fodrin) may crosslink actin proteins of the membrane-associated cytoskeleton. It is a member of a family of actin-cross linking proteins.

[0204] CPS 94 corresponds to ITGA2B which encodes integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B). The gene has LocusID: 3674, and is located on chromosome 17 with reported cytogenetic location 17q21.32. Integrins are heterodimeric integral membrane proteins composed of an alpha chain and a beta chain. Alpha chain 2b undergoes post-translational cleavage to yield disulfide-linked light and heavy chains that join with beta 3 to form a fibronectin receptor expressed in platelets that plays a crucial role in coagulation. Mutations that interfere with this role may result in thrombasthenia. In addition to adhesion, integrins are known to participate in cell-surface mediated signalling. The gene product can act as a receptor for fibrinogen, von Willebrand factor and fibronectin

[0205] CPS 95 corresponds to CTNNAL1 which encodes catenin (cadherin-associated protein), alpha-like 1. The gene has LocusID: 8727, and is located on chromosome 9 with reported cytogenetic location 9q31.2. Alpha-like 1 catenin (cadherin-associated protein) links cadherins to the cytoskeleton. The protein is a member of the catenin family of cadherin-binding proteins.

[0206] CPS 96 corresponds to SCYA2 which encodes small inducible cytokine A2 (monocyte chemotactic protein 1). The gene has LocusID: 6347, and is located on chromosome 17 with reported cytogenetic location 17q11.2-q21.1. Cytokine A2 is a chemotactic factor for monocytes.

[0207] CPS 97 corresponds to NDUFB7 which encodes NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18). The gene has LocusID: 4713, and is located on chromosome 19 with reported cytogenetic location 19p13.12-p13.11. The gene product is a subunit of the NADH-ubiquinone oxidoreductase (complex I).

[0208] CPS 98 corresponds to SCYA7 which encodes small inducible cytokine A7 (monocyte chemotactic protein 3). The gene has LocusID: 6354, and is located on chromosome 17 with reported cytogenetic location 17q11.2-q12. This gene encodes monocyte chemotactic protein 3, a secreted chemokine which attracts macrophages during inflammation and metastasis. It is a member of the C-C subfamily of chemokines which are characterized by having two adjacent cysteine residues. The protein is an *in vivo* substrate of matrix metalloproteinase 2, an enzyme which degrades components of the extracellular matrix. SCYA7 is part of a cluster of C-C chemokine family members on chromosome 17q.

[0209] Nucleotides 1 to 246 of SEQ ID NO: 95 (X72308) have about 95% sequence identity to at least two other genomic sequences. The first genomic sequence is located between the polypeptide-coding sequences of AMPD3 and ZFP26. The second genomic sequence is located near LOC139170. AMPD3 encodes adenosine monophosphate deaminase (isoform E), and has LocusID: 272. The gene is located at chromosome 11p15. ZFP26 encodes C3HC4-like zinc finger protein, and has LocusID: 50862. The gene is located at chromosome 11p15.3. LOC139170 encodes a protein similar to KIAA1892 protein, and is located at chromosome Xq25.

[0210] CPS 99 corresponds to FCGR1A which encodes Fc fragment of IgG, high affinity Ia, receptor for (CD64). The gene has LocusID: 2209, and is located on chromosome 1 with reported cytogenetic location 1q21.2-q21.3. The gene product has a role in immune response, and is a member of the immunoglobulin superfamily.

[0211] CPS 100 corresponds to EPB49 which encodes erythrocyte membrane protein band 4.9 (dematin). The gene has LocusID: 2039, and is located on chromosome 8 with reported cytogenetic location 8p21.1. Dematin may bind to actin. It is a member of the villin family of actin-bundling proteins.

[0212] CPS 101 corresponds to DD96 which encodes epithelial protein up-regulated in carcinoma, membrane associated protein 17. The gene has LocusID: 10158, and is located on chromosome 1 with reported cytogenetic location 1p33. The gene is reported to be up-regulated in malignant epithelial cells of renal cell carcinomas, as well as in carcinomas of colon, breast and lung.

[0213] Nucleotides 1 to 87 of SEQ ID NO: 98 (U21049) show about 98% sequence identity to LOC222094. LOC222094 encodes cell division cycle 2-like 5 (isoform 1), cholinesterase-related cell division controller, and CDC2-related protein kinase 5. It is located at chromosome 7p15.2.

[0214] CPS 102 corresponds to PPARG which encodes peroxisome proliferative activated receptor, gamma. The gene has LocusID: 5468, and is located on chromosome 3 with reported cytogenetic location 3p25. The protein encoded by this gene is a member of the peroxisome proliferator-activated receptor (PPAR) subfamily of nuclear receptors. PPARs form heterodimers with retinoid X receptors (RXRs) and these heterodimers regulate transcription of various genes. Three subtypes of PPARs are known: PPAR-alpha, PPAR-delta, and PPAR-gamma. The protein encoded by this gene is PPAR-gamma and is a regulator of adipocyte differentiation. Additionally, PPAR-gamma has been implicated in the pathology of numerous diseases including obesity, diabetes, atherosclerosis and cancer. Multiple transcript variants that use alternate promoters and splicing have been identified for this gene. At least three of these variants encode the same isoform.

[0215] Nucleotides 1 to 77 of SEQ ID NO: 99 (L40904) have 100% sequence identity to HBA2. HBA2 encodes hemoglobin, alpha 2, and has LocusID: 3040. The gene is located at chromosome 16 with reported cytogenetic location 16p13.3.

[0216] Affymetrix annotation suggests that CPS 103 corresponds to SPINK1. Blast search against the Entrez human genome database shows that CPS 103 also aligns to a genomic sequence between SCGB3A2 and KIAA0555 with at least 97% sequence identity. SCGB3A2 encodes secretoglobin, family 3A, member 2. SCGB3A2 and KIAA0555 are located at chromosome 5q32.

[0217] CPS 104 corresponds to PLAUR which encodes plasminogen activator, urokinase receptor. The gene has LocusID: 5329, and is located on chromosome 19 with reported cytogenetic location 19q13. The gene product, urokinase-type plasminogen activator receptor, may function in pericellular plasminogen activation.

[0218] CPS 105 corresponds to CDC34 which encodes cell division cycle 34. The gene has LocusID: 997, and is located on chromosome 19 with reported cytogenetic location 19p13.3. The protein encoded by this gene is a member of the ubiquitin-conjugating enzyme family. Ubiquitin-conjugating enzyme catalyzes the covalent attachment of ubiquitin to other proteins. CDC34 gene product may be a part of the large multiprotein complex, which is involved in ubiquitin-mediated degradation of cell cycle G1 regulators and the initiation of DNA replication. The gene product is similar to *S. cerevisiae* Cdc34p, and may covalently attach ubiquitin to substrate proteins.

[0219] CPS 106 corresponds to UNK_AI732885 which shows 100% sequence identity with an intron sequence of CG005. CG005 encodes a hypothetical protein from

BCRA2 region. CG005 gene has LocusID: 10443, and is located on chromosome 13 with reported cytogenetic location 13q12-q13. The gene product contains a region having low similarity to a region of rat 2',3'-cyclic nucleotide 3'-phosphodiesterase.

[0220] CPS 107 corresponds to IL10RA which encodes interleukin 10 receptor, alpha. The gene has LocusID: 3587, and is located on chromosome 11 with reported cytogenetic location 11q23. Nucleotides 3467 to 3496 of U00672 have 100% sequence identity to LOC200074 which is located at chromosome 1p34.3.

[0221] CPS 108 corresponds to FBXO7 (FBX7) which encodes F-box only protein 7. The gene has LocusID: 25793, and is located on chromosome 22 with reported cytogenetic location 22q12-q13. This gene encodes a member of the F-box protein family which is characterized by an approximately 40 amino acid motif, the F-box. The F-box proteins constitute one of the four subunits of the ubiquitin protein ligase complex called SCFs (SKP1-cullin-F-box), which functions in phosphorylation-dependent ubiquitination. The F-box proteins are divided into 3 classes: Fbws containing WD-40 domains, Fbls containing leucine-rich repeats, and Fbxs containing either different protein-protein interaction modules or no recognizable motifs. The protein encoded by FBXO7 belongs to the Fbxs class and it may play a role in regulation of hematopoiesis. Alternatively spliced transcript variants of this gene have been reported, but the full length nature of the variants has not been defined.

[0222] CPS 109 corresponds to IFIT4 which encodes interferon-induced protein with tetratricopeptide repeats 4. The gene has LocusID: 3437, and is located on chromosome 10 with reported cytogenetic location 10q24.

[0223] CPS 110 corresponds to BAX which encodes BCL2-associated X protein. The gene has LocusID: 581, and is located on chromosome 19 with reported cytogenetic location 19q13.3-q13.4. The protein encoded by this gene belongs to the BCL2 protein family. BCL2 family members form hetero- or homodimers and act as anti- or pro-apoptotic regulators that are involved in a wide variety of cellular activities. BAX gene product forms a heterodimer with BCL2, and may function as an apoptotic activator. This gene product is reported to interact with, and increase the opening of, the mitochondrial voltage-dependent anion channel (VDAC), which leads to the loss in membrane potential and the release of cytochrome c. The expression of this gene is regulated by the tumor suppressor P53 and has been shown to be involved in P53-mediated apoptosis. Six alternatively spliced transcript variants, which encode different isoforms, have been

reported for this gene. The gene product may induce caspase activation by increasing mitochondrial permeability, and may function in cooperation with the adenine nucleotide translocator (ANT).

[0224] CPS 111 corresponds to BSG which encodes basigin (OK blood group). The gene has LocusID: 682, and is located on chromosome 19 with reported cytogenetic location 19p13.3. Basigin (also known as tumor cell-derived collagenase stimulatory factor, extracellular matrix metalloproteinase inducer, M6 antigen) may stimulate matrix metalloproteinase synthesis in fibroblasts. It is a member of the immunoglobulin superfamily.

[0225] CPS 111 also aligns to LOC199717 with over 97% sequence identity. LOC199717 encodes a protein similar to basigin. LOC199717 is located on chromosome 19 with reported cytogenetic location 19p13.3.

[0226] CPS 112 corresponds to THBS1 which encodes thrombospondin 1. The gene has LocusID: 7057, and is located on chromosome 15 with reported cytogenetic location 15q15. Thrombospondin-1 may have a role in blood clotting and in angiogenesis. It is a member of a family of adhesive molecules.

[0227] CPS 113 corresponds to AP1G2 (G2AD) which encodes adaptor-related protein complex 1, gamma 2 subunit. The gene has LocusID: 8906, and is located on chromosome 14 with reported cytogenetic location 14q11.2. Adaptins are important components of clathrin-coated vesicles transporting ligand-receptor complexes from the plasma membrane or from the trans-Golgi network to lysosomes. The adaptin family of proteins is composed of four classes of molecules named alpha, beta-, beta prime- and gamma- adaptins. Adaptins, together with medium and small subunits, form a heterotetrameric complex called an adaptor, whose role may be to promote the formation of clathrin-coated pits and vesicles. The protein encoded by this gene is a gamma-adaptin protein which belongs to the adaptor complexes large subunits family. Gamma-adaptin is thought to function at some trafficking step in the complex pathways between the trans-Golgi network and the cell surface. There are two alternatively spliced transcript variants of this gene encoding the same protein. The gene product can interact with beta-1 adaptin and sigma 1 chain of the AP-1 complex.

[0228] CPS 115 corresponds to RALBP1 which encodes ralA binding protein 1. The gene has LocusID: 10928, and is located on chromosome 18 with reported cytogenetic location 18p11.3. RalA binding protein 1 can interact with the activated Ral.

[0229] CPS 115 also aligns to KIAA1634 with about 99% sequence identity. KIAA1634 encodes KIAA1634 protein, and is located at chromosome 1p12-p11.2. In addition, CPS 115 shows about 89-92% sequence identity to LOC129522, LOC131054 and a genomic sequence on chromosome 2. LOC129522 encodes a protein similar to ralA binding protein 1, and is located at chromosome 2q11.2. LOC131054 encodes a protein similar to ralA binding protein 1, and is located at chromosome 3q27.2. Nucleotides 3565 to 3875 of L42542 have 94% sequence identity to a chromosome-6 genomic sequence which is located near the polypeptide-coding sequence of LOC221511. LOC221511 encodes MHC class II DP3-alpha, and is located at chromosome 6p21.2.

[0230] CPS 116 corresponds to UNK_AF070587 which is located in an intron of the putative gene LOC196932. LOC196932 gene encodes a protein similar to hypothetical protein LOC55580. LOC196932 is located on chromosome 14 with reported cytogenetic location 14q32.12.

[0231] Affymetrix annotation suggests that CPS 117 corresponds to DUX1. Blast search against the Entrez human genome database shows that CPS 117 also aligns to LOC200133 and LOC131115 with about 82-86% sequence identity. LOC200133 encodes a protein similar to double homeobox, 4 (double homeobox protein 4). It is located at chromosome 1p31.3. LOC131115 encodes a protein similar to double homeobox protein, and is located at chromosome 3p14.1.

[0232] Nucleotides 1 to 698 of SEQ ID NO: 113 (AJ001481) show about 88% sequence identity to DUX4, LOC201498, a genomic sequence near LOC131308, and a genomic sequence near hypothetical gene LOC132684. DUX4 encodes double homeobox, 4. It has LocusID: 22947, and is located on chromosome 4 with reported cytogenetic location 4q35. LOC201498 encodes a protein similar to FSHD Region Gene 2 protein, and is located on chromosome 18. LOC131308 encodes a protein similar to FSHD Region Gene 2 protein, and is located at chromosome 3p14.1. LOC132684 is located at chromosome 4q35.2.

[0233] CPS 118 corresponds to SLC6A8 which encodes solute carrier family 6 (neurotransmitter transporter, creatine), member 8. The gene has LocusID: 6535, and is located on chromosome X with reported cytogenetic location Xq28. The gene product is a sodium and chloride-dependent creatine transporter. It is a member of neurotransmitter transporter family.

[0234] CPS 118 also has about 95% sequence identity to a genomic region on chromosome 16. This region includes or overlaps genes LOC162151 and LOC146488. LOC146488 encodes a protein similar to disintegrin-like testicular metalloproteinase (EC 3.4.24.-) IVb - crab-eating macaque (fragment). The region has reported cytogenetic location 16p11.1. In addition, CPS 118 has about 95% sequence identity to a genomic sequence which includes or overlaps putative genes LOC204478 and LOC146493. LOC146493 encodes a protein similar to sodium- and chloride-dependent creatine transporter 2 (CT2).

[0235] Nucleotides 13923 to 14462 of SEQ ID NO: 114 (U36341) have about 94% sequence identity to a chromosomal region which is located 5' to CTAG2 and 3' to GAB3. CTAG2 encodes cancer/testis antigen 2, and has LocusID: 30848. It is located at chromosome Xq28. GAB3 encodes GRB2-associated binding protein 3, and has LocusID: 139716. It is also located at chromosome Xq28.

[0236] CPS 119 corresponds to THBD which encodes thrombomodulin. The gene has LocusID: 7056, and is located on chromosome 20 with reported cytogenetic location 20p12-cen. Thrombomodulin can change the procoagulant thrombin into an anticoagulant.

[0237] Nucleotides 3867 to 4212 of SEQ ID NO: 115 (J02973) align to a genomic sequence on chromosome 2 with 97% sequence identity. The genomic sequence is located between LOC200422, which encodes a protein similar to somatostatin receptor, and LOC205172. Both LOC200422 and LOC205172 have reported cytogenetic location 2p12.

[0238] Blast search against the Entrez human genome database shows that SEQ ID NO: 116 (CPS 120) has about 99% sequence identity to the protein-coding strand of LOC203068 which encodes a protein similar to tubulin, beta 5. LOC203068 is located on chromosome 6. In addition, SEQ ID NO: 116 has at least 99% sequence identity with LOC157586 and LOC157584. LOC157586 and LOC157584 encode proteins similar to hypothetical protein DKFZp564N123.1 (human fragment). Both LOC157586 and LOC157584 are located on chromosome 6. SEQ ID NO: 116 (AF141349) also has 97% sequence identity with the protein-coding strand of LOC92755. LOC92755 is located at chromosome 8p21.1.

[0239] Nucleotides 14 to 1586 of SEQ ID NO: 116 have 91% sequence identity to LOC222017 which is located at chromosome 7p14.1. Nucleotides 15 to 1572 of SEQ ID NO: 116 have 87% sequence identity to an intron sequence of SCP2. SCP2 encodes sterol carrier protein 2, and has LocusID: 6342. It is located at chromosome 1p32. Sterol carrier

protein 2 may have a role in regulation of steroidogenesis. Moreover, nucleotides 439 to 1474 of SEQ ID NO: 116 share 85% sequence identity to TUBB5 which encodes tubulin, beta, 5. TUBB5 has LocusID: 10382, and is located at chromosome 19p13.3. Beta 5-tubulin can polymerize to form microtubules, and it is a member of a family of structural proteins. Nucleotides 421 to 1444 of SEQ ID NO: 116 also have 84% sequence identity to TUBB4. TUBB4 encodes tubulin, beta, 4, and has LocusID: 10381. It is located at chromosome 16q24.3. Nucleotides 142 to 1474 of SEQ ID NO: 116 align to LOC139112 with 80% sequence identity. LOC139112 encodes a protein similar to tubulin beta, and is located at chromosome Xq25.

[0240] CPS 123 corresponds to HBE1 which encodes hemoglobin, epsilon 1. The gene has LocusID: 3046, and is located on chromosome 11 with reported cytogenetic location 11p15.5. The epsilon globin gene (HBE) is expressed in the embryonic yolk sac. Two epsilon chains together with two zeta chains (an alpha-like globin) constitute the embryonic hemoglobin Hb Gower I, and two epsilon chains together with two alpha chains form the embryonic Hb Gower II. Both of these embryonic hemoglobins are normally supplanted by fetal, and later, adult hemoglobin. The five beta-like globin genes are found within a 45 kb cluster on chromosome 11 in the following order: 5'-epsilon -- G-gamma -- A-gamma -- delta -- beta-3'. Hemoglobin epsilon 1 (embryonic beta-like) can transport oxygen and carbon dioxide between the lung and tissues, and modulate erythrocyte metabolism and senescence.

[0241] CPS 125 corresponds to MAD which encodes MAX dimerization protein. The gene has LocusID: 4084, and is located on chromosome 2 with reported cytogenetic location 2p13-p12. MAX dimerization protein belongs to a subfamily of MAX-interacting proteins. MAD gene product competes with MYC for binding to MAX to form a sequence-specific DNA-binding complex. MAD gene product may act as a transcriptional repressor while MYC appears to function as an activator. MAD gene product is a candidate tumor suppressor gene. The gene product is a basic helix-loop-helix, leucine zipper protein that dimerizes with MAX, and can form a heterodimer with MAX and repress transcription. The gene product may also antagonize c-Myc (MYC) and promote cellular differentiation.

[0242] CPS 126 corresponds to TSPAN-5 which encodes tetraspan 5. The gene has LocusID: 10098, and is located on chromosome 4 with reported cytogenetic location 4q23. The protein encoded by this gene is a member of the transmembrane 4 superfamily, also known as the tetraspanin family. A lot of members in the superfamily are cell-surface

proteins that are characterized by the presence of four hydrophobic domains. These proteins may mediate signal transduction events involved in the regulation of cell development, activation, growth and motility.

[0243] CPS 127 corresponds to BAG1 which encodes BCL2-associated athanogene. The gene has LocusID: 573, and is located on chromosome 9 with reported cytogenetic location 9p12. The oncogene BCL2 is a membrane protein that blocks a step in a pathway leading to apoptosis or programmed cell death. The BAG1 protein binds to BCL2 and is referred to as BCL2-associated athanogene. BAG1 enhances the anti-apoptotic effects of BCL2 and represents a link between growth factor receptors and anti-apoptotic mechanisms. BAG1 interacts with both the hepatocyte growth factor receptor and the platelet-derived growth factor receptor and, in both cases, enhances growth factor-mediated protection from apoptosis. At least three proteins, BAG-1L, BAG-1M and BAG-1, are encoded by the BAG-1 mRNA through the use of alternative translation initiation sites.

[0244] Nucleotides 454 to 1006 of SEQ ID NO: 120 (Z35491) have 88% sequence identity to a chromosomal region on chromosome X. In addition, nucleotides 517 to 646 of SEQ ID NO: 120 align to LOC205900 with 100% sequence identity. LOC205900 encodes a protein similar to serine protease inhibitor Kazal-type 4 precursor (Peptide PEC-60 homolog). LOC205900 is located on chromosome 4.

[0245] CPS 128 corresponds to PADI2 (PDI2) which encodes peptidyl arginine deiminase, type II. The gene has LocusID: 11240, and is located on chromosome 1 with reported cytogenetic location 1p35.2-p35.1. The gene product is similar to rat skeletal muscle peptidyl arginine deiminase, type II, and may convert arginine residues within proteins to citrulline residues.

[0246] Nucleotides 3315 to 4119 of SEQ ID NO: 121 (AB023211) align with PRKG1 with 79% sequence identity. PRKG1 encodes protein kinase, cGMP-dependent, type I, and has LocusID: 5592. Type I cGMP-dependent protein kinase may relax vascular smooth muscle and inhibit platelet aggregation. The gene is located at chromosome 10q11.2. Nucleotides 1375 to 1500 of SEQ ID NO: 121 have 85% sequence identity with PADI1 which encodes peptidyl arginine deiminase, type I. PADI1 has LocusID: 29943, and is located on chromosome 1 with reported cytogenetic location 1p36.13.

[0247] CPS 129 corresponds to IL1R1 which encodes interleukin 1 receptor, type I. The gene has LocusID: 3554, and is located on chromosome 2 with reported cytogenetic

location 2q12. Type I interleukin-1 receptor can bind all three forms of interleukin-1 (IL1A, IL1B, and IL1RN). The protein contains immunoglobulin domains.

[0248] CPS 130 corresponds to NP which encodes nucleoside phosphorylase. The gene has LocusID: 4860, and is located on chromosome 14 with reported cytogenetic location 14q13.1. NP encodes the enzyme purine nucleoside phosphorylase. The encoded protein, together with adenosine deaminase (ADA), serves a key role in purine catabolism, which is referred to as the salvage pathway. Mutations in the encoded protein may result in a severe combined immunodeficiency (SCID).

[0249] CPS 131 corresponds to the 3' untranslated region of AQP3 which encodes aquaporin 3. The gene has LocusID: 360, and is located on chromosome 9 with reported cytogenetic location 9p13. CPS 131 is located in the 3' untranslated region of AQP3. Aquaporin 3 is a water channel protein. Aquaporins are a family of small integral membrane proteins related to the major intrinsic protein (MIP or AQP0). Aquaporin 3 is localized at the basal lateral membranes of collecting duct cells in the kidney. In addition to its water channel function, aquaporin 3 has been found to facilitate the transport of nonionic small solutes such as urea and glycerol, but to a smaller degree. It has been suggested that water channels can be functionally heterogeneous and possess water and solute permeation mechanisms.

[0250] CPS 132 corresponds to GSPT1 which encodes G1 to S phase transition 1. The gene has LocusID: 2935, and is located on chromosome 16 with reported cytogenetic location 16p13.1. The gene product is a GTP-binding protein, and has GTP-binding activity. The product is similar to polypeptide chain elongation factor EF1 alpha (EEF1A1) and may have a role in G1 to S phase transition.

[0251] CPS 132 has about 85% sequence identity with LOC120337. LOC120337 encodes a protein similar to G1 to S phase transition protein 1 homolog (GTP-binding protein GST1-HS). LOC120337 is located at chromosome 11q22.3. Nucleotides 2301 to 2587 of X17644 align with a genomics sequence located 5' to GNB2 with sequence identity of 83%. GNB2 encodes guanine nucleotide binding protein (G protein), beta polypeptide 2. GNB2 has LocusID: 2783, and is located on chromosome 7 with reported cytogenetic location 7q22. Nucleotides 291 to 576 and 585 to 2494 of SEQ ID NO: 125 (X17644) have 82-87% sequence identity with GSPT2 which encodes G1 to S phase transition 2. GSPT2 has LocusID: 23708, and is located on chromosome 5. Nucleotides 2522 to 2587 of SEQ ID NO: 125 have 93% sequence identity with an intron sequence of LOC153643.

LOC153643 encodes a protein similar to hypothetical protein FLJ14957, and is located at chromosome 5q21.1.

[0252] CPS 133 corresponds to GABARAPL2 (GEF-2) which encodes GABA(A) receptor-associated protein-like 2. The gene has LocusID: 11345, and is located on chromosome 16 with reported cytogenetic location 16q22.3-q24.1. The gene product is a phosphoprotein and contains putative actin and nucleotide binding sites. The alternative names for the gene product include GEF2 or ganglioside expression factor 2.

[0253] CPS 133 also has about 81-82% sequence identity with a genomic sequence located 3' to LOC206774, and an intron sequence of RAB3-GAP150. LOC206774 is located at chromosome 8q24.12. RAB3-GAP150 encodes the non-catalytic subunit (150kD) of the rab3 GTPase-activating protein. RAB3-GAP150 has LocusID: 25782, and is located at chromosome 1q42.12. Nucleotides 26 to 253 of SEQ ID NO: 126 (AI565760) have about 84% sequence identity with an intron sequence of ACCN1. ACCN1 encodes amiloride-sensitive cation channel 1, neuronal (degenerin). ACCN1 has LocusID: 40, and is located at chromosome 17q11.2-q12.

[0254] CPS 134 corresponds to HBD which encodes hemoglobin, delta. The gene is located on chromosome 11 with reported cytogenetic location 11p15.5. The gene has LocusID: 3043. HBB, which encodes hemoglobin, beta, is also located in this chromosomal region. The alpha (HBA) and beta (HBB) loci determine the structure of the 2 types of polypeptide chains in adult hemoglobin, Hb A. The normal adult hemoglobin tetramer consists of two alpha chains and two beta chains. Mutant beta globin causes sickle cell anemia. Absence of beta chain causes beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. The order of the genes in the beta-globin cluster is 5'-epsilon -- gamma-G -- gamma-A -- delta -- beta-3'.

[0255] A fragment of CPS 134 (nucleotides 2 to 366 of SEQ ID NO: 127) aligns to HBB with 93-96% sequence identity. Moreover, another fragment of CPS 134 (nucleotides 157 to 364 of SEQ ID NO: 127) has 80% sequence identity with HBE1. HBE1 encodes hemoglobin, epsilon 1. It has LocusID: 3046, and is located at chromosome 11p15.5.

[0256] CPS 135 corresponds to HAGH which encodes hydroxyacyl glutathione hydrolase. The gene has LocusID: 3029, and is located on chromosome 16 with reported cytogenetic location 16p13.3. The enzyme encoded by this gene is classified as a thiolesterase and is responsible for the hydrolysis of S-lactoyl-glutathione to reduced glutathione and D-lactate.

[0257] CPS 136 corresponds to ERN1 which encodes ER to nucleus signalling 1. The gene has LocusID: 2081, and is located on chromosome 17. The gene product is a human homolog of the yeast Ire1 gene product. The ERN1 protein is important in altering gene expression as a response to endoplasmic reticulum based stress signals. The ERN1 protein is a transmembrane endoplasmic reticulum protein, and may act as a sensor of the unfolded protein response pathway.

[0258] Nucleotides 1504 to 1536 of SEQ ID NO: 129 (AF059198) have 96% sequence identity with a chromosomal region on chromosome 3. The region is near LOC152282 which encodes a protein similar to homeobox protein goosecoid. LOC152282 is located at chromosome 3p25.1.

[0259] CPS 137 corresponds to COL9A1 which encodes collagen, type IX, alpha 1. The gene has LocusID: 1297, and is located on chromosome 6 with reported cytogenetic location 6q12-q14. This gene encodes one of the three alpha chains of type IX collagen, a major collagen component of hyaline cartilage. Type IX collagen is usually found in tissues containing type II collagen, a fibrillar collagen. Studies in knockout mice have shown that synthesis of the alpha 1 chain is essential for assembly of type IX collagen molecules, a heterotrimeric molecule, and that lack of type IX collagen is associated with early onset osteoarthritis. Mutations in this gene may be associated with multiple epiphyseal dysplasia. Two transcript variants have been identified for this gene.

[0260] CPS 138 corresponds to S100A11 which encodes S100 calcium binding protein A11 (calgizzarin). The gene has LocusID: 6282, and is located on chromosome 1 with reported cytogenetic location 1q21. The protein encoded by this gene is a member of the S100 family of proteins containing 2 EF-hand calcium-binding motifs. S100 proteins are localized in the cytoplasm and/or nucleus of a wide range of cells, and may be involved in the regulation of a number of cellular processes such as cell cycle progression and differentiation. S100 genes include at least 13 members which are located as a cluster on chromosome 1q21. S100A11 gene product may function in motility, invasion, and tubulin polymerization. Chromosomal rearrangements and altered expression of S100A11 have been implicated in tumor metastasis. Alternative splicing of the 5' UTR of S100A11 results in two gene products.

[0261] CPS 138 also has about 88-90% sequence identity with S100A14, LOC222128, LOC202763 and a genomic sequence containing LOC221948. S100A14 encodes S100 calcium binding protein A14 (calgizzarin). S100A14 has LocusID: 30013,

and is located at chromosome 7q22-q31.1. S100A14 gene product is similar to human calgranulin C protein, and may belong to S100 protein family. LOC222128 encodes protein dpy-19, and is located at chromosome 7p15.3. LOC221948 encodes calgizzarin (S100C protein) (MLN 70), and is located at chromosome 7p22.3. LOC202763 encodes a protein similar to protein dpy-19, and is located on chromosome 17. Nucleotides 103 to 149 of SEQ ID NO: 131 (D38583) align with a genomic sequence on chromosome X with over 90% sequence identity.

[0262] CPS 139 corresponds to FKBP1B which encodes FK506 binding protein 1B (12.6 kD). The gene has LocusID: 2281, and is located on chromosome 2 with reported cytogenetic location 2p23.3. The protein encoded by this gene is a member of the immunophilin protein family. This family of proteins may play a role in immunoregulation and basic cellular processes involving protein folding and trafficking. FKBP1B gene product is a cis-trans prolyl isomerase that can bind the immunosuppressants FK506 and rapamycin. It is similar to the FK506-binding protein 1A. Its physiological role is thought to be in the excitation-contraction coupling in cardiac muscle. There are at least two alternatively spliced transcript variants of this gene encoding different isoforms.

[0263] CPS 139 also has about 83% sequence identity with an intron sequence of LOC145581. LOC145581 encodes a protein similar to hypothetical protein MGC2656, and is located at chromosome 14q13.3.

[0264] CPS 141 corresponds to RNAH which encodes RNA helicase family. The gene has LocusID: 10973, and is located on chromosome 6 with reported cytogenetic location 6q16. CPS 141 is located in the 3' untranslated region of the gene.

[0265] CPS 142 corresponds to MYL9 (MYRL2) which encodes myosin, light polypeptide 9, regulatory. The gene has LocusID: 10398, and is located on chromosome 20 with reported cytogenetic location 20q11.22. The gene product is also known as myosin regulatory light chain 2. The gene product may regulate ATPase activity of myosin heads, and is a member of a protein family that regulates myosin activity.

[0266] CPS 143 corresponds to SPOP which encodes speckle-type POZ protein. The gene has LocusID: 8405, and is located on chromosome 17 with reported cytogenetic location 17q22. The gene product is an autoantigenic protein and may be a DNA or actin binding protein. The product contains a POZ domain, and may mediate protein-protein interactions.

[0267] CPS 144 corresponds to the 3' untranslated region of SLC11A1 which encodes solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1. The gene has LocusID: 6556, and is located on chromosome 2 with reported cytogenetic location 2q35. The gene product is similar to murine Bcg (Nramp1), and may control antimicrobial activity of macrophages.

[0268] CPS 145 corresponds to SIAH2 which encodes seven in absentia homolog 2 (Drosophila). The gene has LocusID: 6478, and is located on chromosome 3 with reported cytogenetic location 3q25. The gene product may be a negative regulator of Vav and DCC mediated signaling pathways.

[0269] CPS 146 corresponds to S100P which encodes S100 calcium binding protein P. The gene has LocusID: 6286, and is located on chromosome 4 with reported cytogenetic location 4p16. The protein encoded by this gene is a member of the S100 family of proteins containing 2 EF-hand calcium-binding motifs. S100 proteins are localized in the cytoplasm and/or nucleus of a wide range of cells, and involved in the regulation of a number of cellular processes such as cell cycle progression and differentiation. S100 genes include at least 13 members which are located as a cluster on chromosome 1q21. However, S100P is located at chromosome 4p16. S100P protein, in addition to binding Ca^{2+} , also binds Zn^{2+} and Mg^{2+} . This protein may play a role in the etiology of prostate cancer.

[0270] CPS 147 corresponds to TNNT1 which encodes troponin T1, skeletal, slow. The gene has LocusID: 7138, and is located on chromosome 19 with reported cytogenetic location 19q13.4. The gene product is also known as troponin T1, tropomyosin-binding subunit of troponin, or slow twitch skeletal muscle regulatory protein.

[0271] Nucleotides 15639 to 15571 of SEQ ID NO: 139 (AJ011712) have 84% sequence identity with a chromosomal region at 4q32.3. Nucleotides 15562 to 15604 of SEQ ID NO: 139 have 93% sequence identity with a chromosomal region near TRAF6. TRAF6 encodes TNF receptor-associated factor 6, and has LocusID: 7189. TRAF6 is located at chromosome 11p11.2.

[0272] CPS 148 corresponds to KIAA0750 which encodes KIAA0750 gene product. The gene has LocusID: 9645, and is located on chromosome 11 with reported cytogenetic location 11p15.2.

[0273] CPS 149 corresponds to FOS which encodes v-fos FBJ murine osteosarcoma viral oncogene homolog. The gene has LocusID: 2353, and is located on chromosome 14 with reported cytogenetic location 14q24.3. The Fos gene family consists of at least four

members: FOS, FOSB, FOSL1, and FOSL2. These genes encode leucine zipper proteins that can dimerize with proteins of the JUN family, thereby forming the transcription factor complex AP-1. As such, the FOS proteins have been implicated as regulators of cell proliferation, differentiation, and transformation. In some cases, expression of the FOS gene has been associated with apoptotic cell death. FOS gene product may function as a transcription factor. It may also be involved in regulation of DNA methylation. The chromosomal region that aligns with CPS 149 also contains LOC196923. LOC196923 encodes a protein similar to proto-oncogene protein c-fos (cellular oncogene fos) (G0/G1 switch regulatory protein 7).

[0274] Nucleotides 1 to 6210 of SEQ ID NO: 141 (K00650) also align with a chromosomal region on chromosome 14 with 99% sequence identity. This chromosomal region includes LOC196937, LOC196936 and LOC196935. All of these three putative genes have reported cytogenetic location 14q23.2. LOC196936 encodes a protein similar to proto-oncogene protein c-fos (cellular oncogene fos) (G0/G1 switch regulatory protein 7). LOC196935 encodes a protein similar to proto-oncogene protein c-fos (cellular oncogene fos) (G0/G1 switch regulatory protein 7).

[0275] CPS 150 corresponds to SERPINB2 (PAI2) which encodes serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2. The gene has LocusID: 5055, and is located on chromosome 18 with reported cytogenetic location 18q21.3. The gene product is known as plasminogen activator inhibitor, type II (arginine-serpin). It is a member of the serpin family of serine protease inhibitors. Alternative names for this gene product include PAI or PLANH2.

[0276] CPS 151 corresponds to PDXK which encodes pyridoxal (pyridoxine, vitamin B6) kinase. The gene has LocusID: 8566, and is located on chromosome 21 with reported cytogenetic location 21q22.3.

[0277] CPS 152 can be derived from homo sapiens mRNA or cDNA DKFZp564D113 (from clone DKFZp564D113). CPS 152 corresponds to a hypothetical gene UNK_AL049250 which represents gene or genes that produce the RNA transcripts capable of hybridizing under stringent conditions to CPS 152. CPS 152 aligns to various chromosomal regions with 97-98% sequence identity. One region includes LOC196123 which is located in an intron sequence of LOC143518. LOC143518 is located on chromosome 11. Another region is located at chromosome 16p12.1 and includes or overlaps LOC146384, LOC197204, and LOC146136. LOC146136 encodes a protein

similar to nuclear pore complex interacting protein. A third region is also located at chromosome 16p12.1, and overlaps LOC220548 which encodes hypothetical protein KIAA0220. A fourth region is next to KIAA0220 which encodes KIAA0220 protein and is located at chromosome 16p12.1. A fifth region is at 16p12.2, and next to LOC146172. A sixth region is on chromosome 7 and includes or overlaps LOC202736, LOC154729, and LOC154725. LOC154729 encodes a protein similar to nuclear pore complex interacting protein. LOC154725 encodes a protein similar to hypothetical protein KIAA0220. A seventh region is near LOC146385 which is located at chromosome 16q13. An eighth region includes LOC197445 which is also located at chromosome 16q13 and encodes a protein similar to BTG3 associated nuclear protein, isoform a (BANP homolog or SMAR1 homolog). A ninth region is at 16q22.3 and includes LOC146452 which encodes a protein similar to KIAA0251 hypothetical protein. A tenth region is at 16p13.2, and aligns with putative gene LOC146613. An eleventh region is located 5' to the polypeptide-coding sequence of NPIP. NPIP encodes a nuclear pore complex interacting protein, and has LocusID: 9284. NPIP is located at chromosome 16p13-p11. Yet another region is located near LOC124155. LOC124155 encodes a protein similar to nuclear pore complex interacting protein, and is located at chromosome 16p11.2. Other regions include LOC197366 at 16p11.2, KIAA0370 at 16p12.1-p11.2, LOC146130 at 16p11.1, and LOC197362 at 16p11.2.

[0278] In addition, CPS 152 has about 97% sequence identity with BANP. BANP encodes BTG3 associated nuclear protein, and has LocusID: 54971. The gene is located at chromosome 18. BTG3 is a protein that interacts with CAF1 which is a component of the general transcription multisubunit complex. It is thought that BTG3 is involved in negative control of the cell cycle. The protein encoded by BANP can bind to BTG3. Studies with mouse homolog suggest that this encoded protein may also interact with a specific nuclear matrix/scaffold-associated region (MAR). Transcript variants encoding different isoforms have been described for BANP gene.

[0279] CPS 152 also aligns with LOC118735 with about 92% sequence identity. LOC118735 encodes a protein similar to apoptosis response protein or prostate apoptosis response protein 4. This gene is located on chromosome 10 with reported cytogenetic location 10q24.2.

[0280] Furthermore, fragments of AL049250 (SEQ ID NO: 144) align with other chromosomal regions with about 78-85% sequence identity. For instance, nucleotides 182

to 2011 of AL049250 align with a genomic sequence near LOC139011. LOC139011 encodes a protein similar to *Arabidopsis thaliana* DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain (JDMU1). LOC139011 is located at chromosome 11p15.5. Nucleotides 1720 to 2185 of SEQ ID NO: 144 (AL049250) align with LOC220178 which has sequence similarity to rat kidney-specific (KS) gene and is located at chromosome 10q23.2. Nucleotides 1463 to 1911 of SEQ ID NO: 144 align with CECR7 which encodes cat eye syndrome chromosome region, candidate 7. CECR7 has LocusID: 27438, and is located on chromosome 22. Moreover, nucleotides 1483 to 1943 of SEQ ID NO: 144 align with LOC204354 which encodes a protein similar to SA rat hypertension-associated homolog and is located on chromosome 15. Nucleotides 1483 to 1943 of SEQ ID NO: 144 align with BUCS1 which encodes butyryl Coenzyme A synthetase 1. BUCS1 has LocusID: 116285, and is located on chromosome 16 with reported cytogenetic location 16p12.2.

[0281] CPS 153 corresponds to GRO2 which encodes GRO2 oncogene. The gene has LocusID: 2920, and is located on chromosome 4 with reported cytogenetic location 4q21. The gene product may be a chemotactic agent for polymorphonuclear leukocytes.

[0282] CPS 153 also aligns with GRO1 with about 85% sequence identity. GRO1 represents GRO1 oncogene (melanoma growth stimulating activity, alpha). The gene has LocusID: 2919, and is located on chromosome 4. The gene product has melanoma growth stimulating activity, and may be a mitogenic factor involved in inflammatory processes.

[0283] In addition, nucleotides 2 to 298 of M36820 (SEQ ID NO: 145) have about 89-94% sequence identity with GRO3. GRO3 represents GRO3 oncogene, and has LocusID: 2921. The gene is located at chromosome 4q21. GRO3 gene product may be a mitogenic factor. Nucleotides 184-299 of SEQ ID NO: 145 (M36820) have 91% sequence identity with LOC201963. LOC201963 encodes a protein similar to heterogeneous nuclear ribonucleoprotein A1 (helix-destabilizing protein) (single-strand binding protein) (hnRNP core protein A1) (HDP). LOC201963 is located at chromosome 4q13.3.

[0284] CPS 154 corresponds to INPP4A which encodes inositol polyphosphate-4-phosphatase, type I, 107kD. The gene has LocusID: 3631, and is located on chromosome 2 with reported cytogenetic location 2q11.2. INPP4A gene product involves in phosphatidylinositol signaling pathways. This product removes the phosphate group at position 4 of the inositol ring from inositol 3,4-bisphosphate.

[0285] CPS 155 corresponds to GPT which encodes glutamic-pyruvate transaminase (alanine aminotransferase). The gene has LocusID: 2875, and is located on chromosome 8 with reported cytogenetic location 8q24.3.

[0286] Nucleotides 9 to 1550 of SEQ ID NO: 147 (U70732) align with a chromosomal region with 96% sequence identity. The chromosomal region is located 3' to FBXL6. FBXL6 encodes F-box and leucine-rich repeat protein 6, and has LocusID: 26233. FBXL6 is located at chromosome 8q24.3. FBXL6 encodes a member of the F-box protein family which is characterized by an approximately 40 amino acid motif, the F-box. Nucleotides 1962 to 2110 of SEQ ID NO: 147 have 83% sequence identity with GPT2 which encodes glutamic pyruvate transaminase (alanine aminotransferase) 2. GPT2 has LocusID: 84706, and is located on chromosome 16.

[0287] CPS 156 corresponds to MYL4 which encodes myosin, light polypeptide 4, alkali; atrial, embryonic. The gene has LocusID: 4635, and is located on chromosome 17 with reported cytogenetic location 17q21-qter. Myosin is a hexameric ATPase cellular motor protein. It is composed of two myosin heavy chains, two nonphosphorylatable myosin alkali light chains, and two phosphorylatable myosin regulatory light chains. MYL4 encodes a myosin alkali light chain that is found in embryonic muscle and adult atria. MYL4 gene product may modulate the interaction between myosin and actin. It is a member of a family of myosin and actin regulatory proteins

[0288] CPS 157 corresponds to NFE2 which encodes nuclear factor (erythroid-derived 2), 45kD. The gene has LocusID: 4778, and is located on chromosome 12 with reported cytogenetic location 12q13. NFE2 gene product is a 45 kD subunit of the bZIP dimeric transcription factor. The transcription factor may regulate expression of the beta globin gene (HBB). CPS 157, as well as NFE2, are located within an intron of ATF7. ATF7 encodes activating transcription factor 7, and has LocusID: 11016. ATF7 is located at chromosome 12q13. The gene product is a leucine zipper DNA-binding protein, and may recognize a cAMP response element (CRE). The gene product may also be involved in the regulation of adenovirus Ela-responsive and cellular cAMP-inducible promoters.

[0289] CPS 158 corresponds to POLR2J which encodes polymerase (RNA) II (DNA directed) polypeptide J (13.3kD). The gene has LocusID: 5439, and is located on chromosome 7 with reported cytogenetic location 7q11.2. This gene encodes a subunit of RNA polymerase II, the polymerase responsible for synthesizing messenger RNA in eukaryotes. The product of this gene exists as a heterodimer with another polymerase

subunit, and the heterodimer forms a core subassembly unit of the polymerase. Two similar genes are located nearby at chromosome 7q11.2 and another similar locus is found at chromosome 7p15.

[0290] Nucleotides 11 to 382 of SEQ ID NO: 150 (L37127) have 94% sequence identity with LOC245815. LOC245815, also known as POLR2J2, is a DNA directed RNA polymerase II polypeptide J-related gene. LOC245815 has LocusID: 246721, and is located at chromosome 7q11.22. Similarity to a related locus suggests that LOC245815 encodes a subunit of RNA polymerase II. Alternative splicing of this gene results in at least three transcript variants encoding different isoforms.

[0291] In addition, nucleotides 11 to 382 of L37127 have 94% sequence identity with a chromosomal region near LOC154696 and a chromosomal region on chromosome 7. LOC154696 encodes a protein similar to HSPC047 protein, and is located at chromosome 7p15.1.

[0292] CPS 159 corresponds to CARM1 which encodes coactivator-associated arginine methyltransferase-1. The gene has LocusID: 10498, and is located on chromosome 19 with reported cytogenetic location 19p13.2.

[0293] CPS 160 corresponds to UNK_AF038171 which is located in an intron sequence of LOC206073. LOC206073 is located on chromosome 4 with reported cytogenetic location 4q24.

[0294] CPS 161 corresponds to RAB2 which encodes RAB2, member RAS oncogene family. The gene has LocusID: 5862, and is located on chromosome 8 with reported cytogenetic location 8q11.23. RAB2 gene product is also known as GTP-binding protein 2, and may be involved in vesicle transport from the ER to the Golgi complex. The gene product is a member of the RAB-subfamily.

[0295] Affymetrix annotation suggests that CPS 162 corresponds to 6H9A. Blast search against the Entrez human genome database shows that CPS 162 aligns with an intron sequence of MYO1E with about 94% sequence identity. MYO1E encodes myosin IE, and has LocusID: 4643. MYO1E is located on chromosome 15 with reported cytogenetic location 15q21-q22. MYO1E gene product is similar to class I myosin, and may bind to proline-rich peptides. The gene product contains an Src homology 3 (SH3) and a myosin head domain (motor domain).

[0296] CPS 163 corresponds to EPB42 which encodes erythrocyte membrane protein band 4.2. The gene has LocusID: 2038, and is located on chromosome 15 with

reported cytogenetic location 15q15-q21. Erythrocyte membrane protein band 4.2 is an ATP-binding protein which may regulate the association of protein 3 with ankyrin. It probably has a role in erythrocyte shape and mechanical property regulation. Mutations in the EPB42 gene are associated with recessive spherocytic elliptocytosis and recessively transmitted hereditary hemolytic anemia.

[0297] CPS 163 also aligns with LOC203401 with about 97% sequence identity. LOC203401 encodes a protein similar to erythrocyte membrane protein band 4.2 (P4.2) (Pallidin). The chromosomal location of LOC203401 is unknown.

[0298] CPS 164 corresponds to CGTHBA which denotes "conserved gene telomeric to alpha globin cluster." The gene has LocusID: 8131, and is located on chromosome 16 with reported cytogenetic location 16p13.3.

[0299] CPS 165 corresponds to DOC-1R which encodes tumor suppressor deleted in oral cancer-related 1. The gene has LocusID: 10263, and is located on chromosome 11 with reported cytogenetic location 11q13. The gene product is similar to hamster doo-1. CPS 165 also aligns with LOC222984 with about 89% sequence identity. LOC222984 encodes a protein similar to tumor suppressor deleted in oral cancer-related 1, and is located at chromosome 7p22.2.

[0300] Nucleotides 3 to 663 of SEQ ID NO: 157 (AF089814) have about 86% sequence identity with LOC169609 and LOC169607. Both genes encode a protein similar to Myosin Vb (Myosin 5B). LOC169609 is located at chromosome 9q12. LOC169607 is located at chromosome 9q21.11. In addition, nucleotides 3 to 777 of AF089814 have about 86-93% sequence identity with LOC138403. LOC138403 encodes a protein similar to Myosin Vb (Myosin 5B), and is located at chromosome 9q13.

[0301] CPS 166 corresponds to KIAA0353 (DMN) which encodes desmuslin. The gene has LocusID: 23336. DMN is located on chromosome 15 with reported cytogenetic location 15q26.3.

[0302] A fragment of CPS 166 (nucleotides 477 to 602 of AI077476) aligns with LOC120511 with about 97% sequence identity. LOC120511 encodes a protein similar to rig-1 protein (mouse), and is located at chromosome 11q23.3.

[0303] Affymetrix annotation suggests that CPS 167 corresponds to CSH1. Blast search against the Entrez human genome database shows that CPS 167 also aligns with CSH2 with about 98% sequence identity. CSH2 encodes chorionic somatomammotropin hormone 2. The gene has LocusID: 1443, and is located on chromosome 17 with reported

cytogenetic location 17q24.2. The protein encoded by this gene is a member of the somatotropin/prolactin family of hormones and may play an important role in growth control. CSH2 is located at the growth hormone locus on chromosome 17 along with four other related genes in the same transcriptional orientation. This arrangement is thought to have evolved by a series of gene duplications. Although the five genes share a high degree of sequence identity, they are reported to be expressed in different tissues. Alternative splicing generates additional isoforms of each of the five growth hormones. CSH2 is expressed in the placenta and utilizes multiple transcription initiation sites. Expression of the mature proteins for chorionic somatomammotropin hormones 1 and 2 is upregulated during development.

[0304] CPS 168 corresponds to LOC51048 (DKK3) which encodes dickkopf homolog 3 (*Xenopus laevis*) (RIG-like 5-6). The gene has LocusID: 27122, and is located on chromosome 11 with reported cytogenetic location 11p15.2. DKK3 gene product is also known as RIG-like 7-1, and may be related to proteins that antagonize Wnt signaling.

[0305] Nucleotides 3 to 92 of SEQ ID NO: 160 (AF034209) have about 90% sequence identity with RIG (regulated in glioma). RIG has LocusID: 10530, and is located at chromosome 11p15.1.

[0306] CPS 169 corresponds to SELP which encodes selectin P (granule membrane protein 140kD, antigen CD62). The gene has LocusID: 6403, and is located on chromosome 1 with reported cytogenetic location 1q22-q25. SELP gene product is a platelet alpha-granule membrane protein of molecular weight 140,000 that redistributes to the plasma membrane during platelet activation and degranulation. It is a member of a family of adhesion/homing receptors. Alternative splice variants may occur but are not well documented. The gene product may mediate interactions of leukocytes with the blood vessel wall. It contains an EGF domain and complement regulatory (CR) protein domains.

[0307] CPS 170 corresponds to RAP1GA1 which encodes GTPase activating protein 1 for RAP1. The gene has LocusID: 5909, and is located on chromosome 1 with reported cytogenetic location 1p36.1-p35. Nucleotides 916 to 1044 of SEQ ID NO: 162 (M64788) have about 85% identity with KIAA1039. KIAA1039 encodes KIAA1039 protein, and has LocusID: 23108. The gene has reported cytogenetic location 17p13.3.

[0308] CPS 171 corresponds to THBS1 which encodes thrombospondin 1. The gene has LocusID: 7057, and is located on chromosome 15 with reported cytogenetic

location 15q15. Thrombospondin-1 may have a role in blood clotting and in angiogenesis. It is a member of a family of adhesive molecules.

[0309] CPS 172 corresponds to CHRNA4 which encodes cholinergic receptor, nicotinic, alpha polypeptide 4. The gene has LocusID: 1137, and is located on chromosome 20 with reported cytogenetic location 20q13.2-q13.3. Nucleotides 615 to 1995 of SEQ ID NO: 164 (U62433) also align with LOC149656. LOC149656 encodes a protein similar to neuronal acetylcholine receptor protein, alpha-4 chain precursor, and is located at chromosome 20q13.33.

[0310] Fragments of nucleotides 602 to 1313 of U62433 (SEQ ID NO: 164) align with CHRNA2, CHRNA3 and CHRNB2 with about 79-89% sequence identity. CHRNA2 encodes cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal). CHRNA2 has LocusID: 1135, and is located at chromosome 8p21. CHRNA3 encodes cholinergic receptor, nicotinic, alpha polypeptide 3. CHRNA3 has LocusID: 1136, and is located at chromosome 15q24. CHRNB2 encodes cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal). CHRNB2 has LocusID: 1141, and is located at chromosome 1q21.3.

[0311] CPS 173 corresponds to S100A12 which encodes S100 calcium binding protein A12 (calgranulin C). The gene has LocusID: 6283, and is located on chromosome 1 with reported cytogenetic location 1q21. The protein encoded by this gene is a member of the S100 family of proteins containing 2 EF-hand calcium-binding motifs. S100 proteins are localized in the cytoplasm and/or nucleus of a wide range of cells, and involved in the regulation of a number of cellular processes such as cell cycle progression and differentiation. S100 genes include at least 13 members which are located as a cluster on chromosome 1q21. S100A12 gene product is proposed to be involved in specific calcium-dependent signal transduction pathways, and its regulatory effect on cytoskeletal components may modulate various neutrophil activities.

[0312] CPS 174 corresponds to CD9 which encodes CD9 antigen (p24). The gene has LocusID: 928, and is located on chromosome 12 with reported cytogenetic location 12p13.3. The protein encoded by this gene is a member of the transmembrane 4 superfamily, also known as the tetraspanin family. Most of these members are cell-surface proteins that are characterized by the presence of four hydrophobic domains. These proteins mediate signal transduction events that play a role in the regulation of cell development, activation, growth and motility. CD9-encoded protein is a cell surface glycoprotein that is known to complex with integrins and other transmembrane 4

superfamily proteins. It can modulate cell adhesion and migration and also trigger platelet activation and aggregation. In addition, the encoded protein appears to promote muscle cell fusion and support myotube maintenance.

[0313] CPS 175 corresponds to PRDX2 (TDPX1) which encodes peroxiredoxin 2. Peroxiredoxin 2 is also known as thioredoxin-dependent peroxide reductase (thiol-specific antioxidant 1, natural killer-enhancing factor B), and may be protective against oxidative stress. PRDX2 gene has LocusID: 7001, and is located on chromosome 19 with reported cytogenetic location 19p13.2.

[0314] CPS 175 has about 88% sequence identity with MGC2599 and LOC134602. MGC2599 encodes hypothetical protein MGC2599 which is similar to katanin p60 subunit A 1 2599. The gene has LocusID: 84056, and is located at chromosome 13q12.2. LOC134602 encodes a protein similar to thiol-specific antioxidant (TSA), and is located at chromosome 6q21.

[0315] Nucleotides 497 to 767 of SEQ ID NO: 167 (L19185) align with LOC219772 with 89% sequence identity. LOC219772 encodes peroxiredoxin 2 (thioredoxin peroxidase 1) (thioredoxin-dependent peroxide reductase 1) (thiol-specific antioxidant protein) (TSA) (PRP) (Natural killer cell enhancing factor B) (NKEF-B). LOC219772 is located at chromosome 10q11.21. Moreover, nucleotides 5 to 65 of L19185 show 100% sequence identity with LOC204141 and LOC205227. LOC204141 is similar to H-NUC (human), and is located on chromosome 13. LOC205227 encodes a protein similar to malonyl-CoA decarboxylase (EC 4.1.1.9) (goose), and is located on chromosome 2.

[0316] CPS 176 corresponds to B7 which encodes B7 protein. The gene has LocusID: 10233, and is located on chromosome 12 with reported cytogenetic location 12p13. B7 protein has a low sequence similarity to the regulatory subunit of protein phosphatases. B7 protein contains leucine rich repeats, and may mediate protein-protein interactions.

[0317] CPS 177 corresponds to BPGM which encodes 2,3-bisphosphoglycerate mutase. The gene has LocusID: 669, and is located on chromosome 7 with reported cytogenetic location 7q31-q34. 2,3-bisphosphoglycerate mutase has synthase, mutase, and phosphatase activities. It is involved in controlling 2,3-diphosphoglycerate metabolism.

[0318] CPS 178 corresponds to PSMA7 which encodes proteasome (prosome, macropain) subunit, alpha type, 7. The gene has LocusID: 5688, and is located on

chromosome 20 with reported cytogenetic location 20q13.33. Alpha subunit 7 of the proteasome (prosome macropain) is a possible target for hepatitis B virus X protein.

[0319] CPS 179 corresponds to GMPR which encodes guanosine monophosphate reductase. The gene has LocusID: 2766, and is located on chromosome 6 with reported cytogenetic location 6p23. Guanosine monophosphate reductase may facilitate thermogenesis, and has very strong similarity to rat guanosine monophosphate reductase.

[0320] CPS 180 corresponds to TMOD which encodes tropomodulin. The gene has LocusID: 7111, and is located on chromosome 9 with reported cytogenetic location 9q22.3. Tropomodulin can bind to an end of erythrocyte tropomyosin.

[0321] CPS 181 corresponds to C4A which encodes complement component 4A. The gene has LocusID: 720. The gene is located on chromosome 6. This gene encodes the acidic form of complement factor 4, part of the classical activation pathway. The gene product is expressed as a single chain precursor which is proteolytically cleaved into a trimer of alpha, beta, and gamma chains prior to secretion. The trimer provides a surface for interaction between the antigen-antibody complex and other complement components. The alpha chain may be cleaved to release C4 anaphylatoxin, a mediator of local inflammation. Deficiency of complement component 4A is associated with systemic lupus erythematosus and type I diabetes mellitus. C4A gene localizes to the major histocompatibility complex (MHC) class III region on chromosome 6. Varying haplotypes of this gene cluster exist, such that individuals may have 1, 2, or 3 copies of this gene.

[0322] Fragments of CPS 181 (nucleotides 1 to 45 and nucleotides 199 to 248 of SEQ ID NO: 173) also align with LOC220819 with 100% sequence identity. LOC220819 encodes a protein similar to dJ34F7.4 (complement component 4A). LOC220819 is located on chromosome 6.

[0323] In addition, CPS 181 aligns with C4B with over 94% sequence identity. C4B encodes complement component 4B, and has LocusID: 721. C4B is located at chromosome 6p21.3. C4B gene encodes the basic form of complement factor 4, part of the classical activation pathway. This gene exists as a long form and a short form due to the presence or absence of a 6.4 kb endogenous HERV-K retrovirus in intron 9.

[0324] CPS 182 corresponds to GPR12 which encodes G protein-coupled receptor 12. The gene has LocusID: 2835, and is located on chromosome 13 with reported cytogenetic location 13q12. The gene product is a member of the G protein-coupled receptor family. It is similar to murine Gpcr12 and rat Rn.10218.

[0325] CPS 182 also aligns with a sequence near LOC202175 with 97% sequence identity. LOC202175 is located at chromosome 5p15.33.

[0326] CPS 183 corresponds to ADFP which encodes adipose differentiation-related protein. The gene has LocusID: 123, and is located on chromosome 9 with reported cytogenetic location 9p21.2. Adipocyte differentiation-related protein is associated with the globule surface membrane material. This protein is a major constituent of the globule surface. Increase in mRNA levels is one of the earliest indications of adipocyte differentiation. The protein is a component of milk lipid globules. The protein is also known as adipophilin.

[0327] Nucleotides 1 to 1314 of SEQ ID NO: 175 (X97324) have 91-92% sequence identity with ILF2 which encodes interleukin enhancer binding factor 2, 45kD. ILF2 has LocusID: 3608, and is located at chromosome 1q21.1. The gene product is a subunit of nuclear factor of activated T-cells (NF-AT). It is a DNA-binding transcription factor.

[0328] CPS 184 corresponds to MYL5 which encodes myosin, light polypeptide 5, regulatory. The gene has LocusID: 4636, and is located on chromosome 4 with reported cytogenetic location 4p16.3. This gene encodes one of the myosin light chains, a component of the hexameric ATPase cellular motor protein myosin. Myosin is composed of two heavy chains, two nonphosphorylatable alkali light chains, and two phosphorylatable regulatory light chains. This gene product, one of the regulatory light chains, is expressed in fetal muscle and in adult retina, cerebellum, and basal ganglia. The gene product may modulate the interaction between myosin and actin. It is a member of a family of myosin and actin regulatory proteins.

[0329] CPS 185 corresponds to DPM2 which encodes dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit. The gene has LocusID: 8818, and is located on chromosome 9 with reported cytogenetic location 9q34.13.

[0330] CPS 186 corresponds to MCC which encodes a protein mutated in colorectal cancers. The gene has LocusID: 4163, and is located on chromosome 5 with reported cytogenetic location 5q21-q22. MCC is a candidate for the putative colorectal tumor suppressor gene. The MCC gene product may be involved in early stages of colorectal neoplasia in both sporadic and familial tumors. The gene product is similar to the G protein-coupled m3 muscarinic acetylcholine receptor.

[0331] CPS 187 corresponds to F3 which encodes coagulation factor III (thromboplastin, tissue factor). The gene has LocusID: 2152, and is located on

chromosome 1 with reported cytogenetic location 1p22-p21. This gene encodes coagulation factor III which is a cell surface glycoprotein. This factor enables cells to initiate the blood coagulation cascades, and it functions as the high-affinity receptor for the coagulation factor VII. The resulting complex provides a catalytic event that is responsible for initiation of the coagulation protease cascades by specific limited proteolysis. Unlike some of other cofactors of these protease cascades, which circulate as nonfunctional precursors, coagulation factor III is a potent initiator that is fully functional when expressed on cell surfaces. There are 3 distinct domains of this factor: extracellular, transmembrane, and cytoplasmic. Coagulation factor III can initiate the coagulation protease cascade assembly and propagation, and may function in normal hemostasis. The factor is a component of the cellular immune response.

[0332] CPS 188 corresponds to KLF1 which encodes Kruppel-like factor 1 (erythroid). The gene has LocusID: 10661, and is located on chromosome 19 with reported cytogenetic location 19p13.13-p13.12. Erythroid Kruppel-like factor 1 is a transcriptional activator of the adult beta-globin promoter.

[0333] CPS 188 also aligns to LOC146544 with about 94% sequence identity. LOC146544 is located on chromosome 16.

[0334] CPS 189 corresponds to HBG2. HBG2 encodes hemoglobin, gamma G. The gene has LocusID: 3047, and is located on chromosome 11 with reported cytogenetic location 11p15.5. HBG1 is also located in the same chromosomal region. The gamma globin genes (HBG1 and HBG2) are normally expressed in the fetal liver, spleen and bone marrow. Two gamma chains together with two alpha chains constitute fetal hemoglobin (HbF) which is normally replaced by adult hemoglobin (HbA) at birth. In some beta-thalassemias and related conditions, gamma chain production continues into adulthood. The two types of gamma chains differ at residue 136 where glycine is found in the G-gamma product (HBG2) and alanine is found in the A-gamma product (HBG1). The former is predominant at birth. The order of the genes in the beta-globin cluster is: 5'-epsilon -- gamma-G -- gamma-A -- delta -- beta--3'. The gene product(s) can transport oxygen and carbon dioxide between lung and tissues.

[0335] A fragment of CPS 189 (nucleotides 332..234 of SEQ ID NO: 181) has 86% sequence identity with HBE1 which encodes hemoglobin, epsilon 1.

[0336] In addition, SEQ ID NO: 277 (M91036) can be used to design probes for detecting HBG2. Nucleotides 2162-2268, 2391-2614 and 3501-3565 of SEQ ID NO: 277

align to HBG2 with 100% sequence identity. Nucleotides 2379 to 2626 and 7309 to 7556 of SEQ ID NO: 277 have 87% sequence identity with HBE1 which encodes hemoglobin, epsilon 1. HBE1 gene has LocusID: 3046, and is located at chromosome 11p15.5. Nucleotides 2384 to 2621 and 7314 to 7551 of SEQ ID NO: 277 also have 84% sequence identity with a chromosomal region on chromosome 11.

[0337] CPS 190 corresponds to GRO3 which encodes GRO3 oncogene. The gene has LocusID: 2921, and is located on chromosome 4 with reported cytogenetic location 4q21. The gene product may be a mitogenic factor.

[0338] Nucleotides 6 to 298 of SEQ ID NO: 182 (M36821) have about 86-95% sequence identity with GRO1 and GRO2. GRO1 encodes GRO1 oncogene (melanoma growth stimulating activity, alpha), and has LocusID: 2919. GRO1 is located at chromosome 4q21. GRO1 gene product has melanoma growth stimulating activity, and may be a mitogenic factor involved in inflammatory processes. GRO2 encodes GRO2 oncogene, and has LocusID: 2920. GRO2 is located at chromosome 4q21. GRO2 gene product may be a chemotactic agent for polymorphonuclear leukocytes.

[0339] Affymetrix annotation suggests that CPS 191 corresponds to PLEC1. Blast search against the Entrez human genome database shows that nucleotides 14629 to 14800 of SEQ ID NO: 183 (U53204) have 93% sequence identity with LOC162613 and a chromosomal region near LOC93232. Both LOC162613 and LOC93232 are located at chromosome 17q25.3, and encode proteins similar to KIAA1640 protein. In addition, nucleotides 14268 to 14800 of SEQ ID NO: 183 (U53204) align with LOC160535 with 88% sequence identity. LOC160535 is located at chromosome 12q12.

[0340] CPS 192 corresponds to SLC16A3 which encodes solute carrier family 16 (monocarboxylic acid transporters), member 3. The gene has LocusID: 9123, and is located on chromosome 17. The gene product is a member of monocarboxylate transporter family, and may function as a transporter. Nucleotides 34 to 945 of SEQ ID NO: 184 (U81800) align with LOC201281 with over 96% sequence identity. LOC201281 encodes a protein similar to monocarboxylate transporter, and is located at chromosome 17q25.3.

[0341] CPS 194 corresponds to FKBP8 which encodes FK506 binding protein 8 (38kD). The gene has LocusID: 23770, and is located on chromosome 19 with reported cytogenetic location 19p12. The protein encoded by this gene is a member of the immunophilin protein family, which play a role in immunoregulation and basic cellular processes involving protein folding and trafficking. The encoded protein does not seem to

have PPIase/rotamase activity. It has a three-unit tetratricopeptide repeat and a consensus leucine-zipper repeat, and may have a role in neurons associated with memory function.

[0342] CPS 194 also aligns with an intron sequence of PPP1R12B with about 88% sequence identity. PPP1R12B encodes protein phosphatase 1, regulatory (inhibitor) subunit 12B. The gene has LocusID: 4660, and is located on chromosome 1 with reported cytogenetic location 1q32.1. Myosin light chain phosphatase (MLCP) consists of three subunits: the catalytic subunit, the large subunit/myosin binding subunit (MBS) and the small subunit (sm-M20). PPP1R12B is a multi-functional gene which encodes both MBS and sm-M20. MLCP regulates myosins and the dephosphorylation is enhanced by the presence of MBS. The sm-M20 subunit is suggested to play a regulatory role in muscle contraction by binding to MBS. MBS is also encoded by another gene, myosin light chain phosphatase target subunit 1. Although both MBSs increase the activity of MLCP, myosin light chain phosphatase target subunit 1-MBS is a more efficient activator. There are at least four alternatively spliced transcript variants of PPP1R12B described, two altering the MBS coding region and two altering the sm-M20 coding region.

[0343] CPS 195 corresponds to RNASE2 which encodes ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin). The gene has LocusID: 6036, and is located on chromosome 14 with reported cytogenetic location 14q24-q31. Eosinophil-derived neurotoxin has neurotoxic and ribonuclease activities. It is a member of the ribonuclease superfamily.

[0344] CPS 195 also aligns with LOC122661 with about 92% sequence identity. LOC122661 encodes a protein similar to nonsecretory ribonuclease precursor (ribonuclease US) (eosinophil-derived neurotoxin) (RNase UpI-2) (ribonuclease 2) (RNase 2). LOC122661 is located at chromosome 14q11.1. In addition, CPS 195 has about 88-94% sequence identity with RNASE3. RNASE3 encodes ribonuclease, RNase A family, 3 (eosinophil cationic protein). RNASE3 has LocusID: 6037, and is located at chromosome 14q24-q31. RNASE3 gene product has neurotoxic and ribonuclease activities. It is a member of the ribonuclease superfamily.

[0345] Nucleotides 639 to 735 of SEQ ID NO: 186 (X55988) show 95% sequence identity with an intron sequence of LOC159655. LOC159655 is located at chromosome 10q23.33.

[0346] CPS 196 corresponds to BCAT1 which encodes branched chain aminotransferase 1, cytosolic. The gene has LocusID: 586, and is located on chromosome

12 with reported cytogenetic location 12pter-q12. The lack of the cytosolic enzyme branched-chain amino acid transaminase (BCT) causes cell growth inhibition. There may be 2 different clinical disorders due to a defect of branched-chain amino acid transamination: hypervalinemia and hyperleucine-isoleucinemia. Cytosolic branched-chain amino acid aminotransferase 1 catalyzes conversion of branched-chain α -keto acids to L-amino acids.

[0347] CPS 199 corresponds to SPP1 which encodes secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1). The gene has LocusID: 6696, and is located on chromosome 4 with reported cytogenetic location 4q21-q25. Osteopontin (bone sialoprotein) is a bone and blood vessel extracellular matrix protein involved in calcification and atherosclerosis.

[0348] CPS 201 corresponds to GRO1 which encodes GRO1 oncogene (melanoma growth stimulating activity, alpha). The gene has LocusID: 2919, and is located on chromosome 4 with reported cytogenetic location 4q21. The gene product has melanoma growth stimulating activity, and may be a mitogenic factor involved in inflammatory processes.

[0349] CPS 201 also aligns with GRO2, which encodes GRO2 oncogene, with 87-89% sequence identity. GRO2 has LocusID: 2920, and is located at chromosome 4q21. GRO2 may be a chemotactic agent for polymorphonuclear leukocytes.

[0350] Nucleotides 1 to 830 of SEQ ID NO: 189 (X54489) have about 90% sequence identity with GRO3 which encodes GRO3 oncogene. GRO3 has LocusID: 2921, and is located at chromosome 4q21. GRO3 gene product may be a mitogenic factor. Nucleotides 2 to 466 of SEQ ID NO: 189 have 85% sequence identity with LOC201963 which encodes a protein similar to heterogeneous nuclear ribonucleoprotein A1 (helix-destabilizing protein) (single-strand binding protein) (hnRNP core protein A1) (HDP). LOC201963 is located at chromosome 4q13.3.

[0351] CPS 202 corresponds to FLJ21588 (DKFZP586O0223) which encodes ASC-1 complex subunit P100. The gene has LocusID: 84164, and is located on chromosome 22 with reported cytogenetic location 22q12.1.

[0352] CPS 205 corresponds to FASN which encodes fatty acid synthase. The gene has LocusID: 2194, and is located on chromosome 17 with reported cytogenetic location 17q25. The enzyme encoded by this gene is a multifunctional protein. One of its functions is to catalyze the synthesis of palmitate from acetyl-CoA and malonyl-CoA, in the presence

of NADPH, into long-chain saturated fatty acids. In some cancer cell lines, this protein has been found to be fused with estrogen receptor-alpha (ER-alpha), in which the N-terminus of FAS is fused in-frame with the C-terminus of ER-alpha.

[0353] Nucleotides 7777 to 8199 and 8270 to 8457 of SEQ ID NO: 192 (U29344) have about 94-96% sequence identity with LOC133934. The gene is a hypothetical gene, and is located at chromosome 5p15.2. Nucleotides 7528 to 8223 of SEQ ID NO: 192 show 84% sequence identity with an intron sequence of LY9 which encodes lymphocyte antigen 9. LY9 has LocusID: 4063, and is located at chromosome 1q21.3-q22. Lymphocyte antigen 9 may be involved in adhesion between T cells and accessory cells. It is a member of the immunoglobulin superfamily. In addition, nucleotides 8299 to 8337 of U29344 align with DDX27 with 97% sequence identity. DDX27 encodes DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 27, and has LocusID: 55661. DDX27 is located at chromosome 20q13.13. DEAD box proteins, characterized by the conserved motif Asp-Glu-Ala-Asp (DEAD), are putative RNA helicases. They are implicated in a number of cellular processes involving alteration of RNA secondary structure such as translation initiation, nuclear and mitochondrial splicing, and ribosome and spliceosome assembly. Based on their distribution patterns, some members of this family are believed to be involved in embryogenesis, spermatogenesis, and cellular growth and division. DDX27 encodes a DEAD box protein which is a member of the DEAD/DEAH box ATP-dependent RNA or DNA helicase family.

[0354] CPS 206 corresponds to HOXA1 which encodes homeo box A1. The gene has LocusID: 3198, and is located on chromosome 7 with reported cytogenetic location 7p15.3. Homeo box A1 is a member of homeodomain family of DNA binding proteins, and may regulate gene expression, morphogenesis, and differentiation.

[0355] CPS 207 corresponds to HMOX1 which encodes heme oxygenase (decycling) 1. The gene has LocusID: 3162, and is located on chromosome 22 with reported cytogenetic location 22q13.1. CPS 207 aligns with nucleotides 15085942 to 15086457 of chromosome 22 with 100% sequence identity. Heme oxygenase, an essential enzyme in heme catabolism, cleaves heme to form biliverdin, which is subsequently converted to bilirubin by biliverdin reductase, and carbon monoxide, a putative neurotransmitter. Heme oxygenase activity is induced by its substrate heme and by various nonheme substances. Heme oxygenase occurs as 2 isozymes, an inducible heme

oxygenase-1 and a constitutive heme oxygenase-2. HMOX1 and HMOX2 belong to the heme oxygenase family.

[0356] The chromosomal region to which CPS 207 aligns is in the proximity of other genes. These genes include MCM5 and LOC129121. MCM5 encodes MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (*S. cerevisiae*). It is LocusID: 4174, and located at chromosome 22q13.1. The protein encoded by MCM5 is similar to *S. cerevisiae* CDC46 which is involved in the initiation of DNA synthesis. MCM5 gene product is a member of the MCM family of chromatin-binding proteins. LOC129121 is a hypothetical gene LOC129121 which is located at chromosome 22q12.3.

[0357] Nucleotides 26880 to 28079 of SEQ ID NO: 194 (Z82244) align with LOC168550 with 79% sequence identity. LOC168550 encodes a protein similar to pol protein. LOC168550 is located at chromosome 7q36.1. Nucleotides 26774 to 28057 of SEQ ID NO: 194 align with LOC205176 with 76% sequence identity. LOC205176 is located at chromosome 2p12.

[0358] Affymetrix annotation suggests that CPS 208 corresponds to BNIP3. Blast search against the Entrez human genome database shows that CPS 208 also aligns with LOC159348 with over 98% sequence identity. LOC159348 is located on chromosome 10 with reported cytogenetic location 10q26.3. In addition, CPS 208 aligns with a chromosomal region on chromosome 14 with about 97% sequence identity. CPS 208 also has about 81% sequence identity with an intron sequence of LOC146062. LOC146062 encodes a protein similar to FLJ00088 protein, and is located at chromosome 15q14.

[0359] Nucleotides 152 to 1081 of SEQ ID NO: 195 (AF002697) align with a chromosomal region near LOC152687 with 78% sequence identity. LOC152687 encodes a protein similar to Zinc finger protein 91 (zinc finger protein HTF10) (HPF7), and is located at chromosome 4p16.3.

[0360] CPS 209 corresponds to ZNF261 which encodes zinc finger protein 261. The gene has LocusID: 9203, and is located on chromosome X with reported cytogenetic location Xq13.1. The gene product contains a putative zinc-binding motif (MYM).

[0361] CPS 210 corresponds to MYH7 which encodes myosin, heavy polypeptide 7, cardiac muscle, beta. The gene has LocusID: 4625, and is located on chromosome 14 with reported cytogenetic location 14q12. MYH7 encodes the cardiac muscle beta (or slow) isoform of myosin. Changes in the relative abundance of MYH7 gene product and MYH6 gene product (the alpha, or fast, isoform of cardiac myosin heavy chain) correlate with the

contractile velocity of cardiac muscle. Mutations in MYH7 are associated with familial hypertrophic cardiomyopathy. MYH7 gene product is a member of the motor protein family that provide force for muscle contraction.

[0362] Nucleotides 432 to 5869 of SEQ ID NO: 197 (M58018) align with MYH6 with about 88-98% sequence identity. In particular, nucleotides 5741 to 5869 align with MYH6 with 96% sequence identity. MYH6 encodes myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1). It has LocusID: 4624, and is located at chromosome 14q12. Cardiac myosin heavy chain 6 alpha is a member of motor protein family that provide force for muscle contraction.

[0363] Various fragments in nucleotides 432 to 5543 of M58018 have about 77-90% sequence identity with MYH1, MYH2, MYH3, MYH4 and MYH13. MYH1 encodes myosin, heavy polypeptide 1, skeletal muscle, adult, and has LocusID: 4619. MYH2 encodes myosin, heavy polypeptide 2, skeletal muscle, adult, and has LocusID: 4620. MYH3 encodes myosin, heavy polypeptide 3, skeletal muscle, embryonic, and has LocusID: 4621. MYH4 encodes myosin, heavy polypeptide 4, skeletal muscle, and has LocusID: 4622. MYH13 encodes myosin, heavy polypeptide 13, skeletal muscle, and has LocusID: 8735. MYH1, MYH2, MYH3 and MYH4 are all reportedly located at chromosome 17p13.1. MYH13 has reported cytogenetic location 17p13.

[0364] Myosin is a major contractile protein which converts chemical energy into mechanical energy through the hydrolysis of ATP. Myosin is a hexameric protein composed of a pair of myosin heavy chains (MYH) and two pairs of nonidentical light chains. Myosin heavy chains are encoded by a multigene family. In mammals at least 10 different myosin heavy chain (MYH) isoforms have been described from striated, smooth, and nonmuscle cells. These isoforms show expression that is spatially and temporally regulated during development. The proteins encoded by MYH1, MYH4 and MYH13 contain ATPase head and rod-like tail domains. Myosin heavy chain 1 and 13 may provide force for muscle contraction, cytokinesis and phagocytosis. Skeletal muscle myosin heavy chain 3 and 4 may provide force for muscle contraction.

[0365] In addition, nucleotides 1494 to 1654 of M58018 align with MYH7B and a chromosomal region near FLJ22037 with about 88-92% sequence identity. FLJ22037 encodes hypothetical protein FLJ22037, and has LocusID: 84176. It is located on chromosome 7 with reported cytogenetic location 7q11.21. MYH7B encodes myosin,

heavy polypeptide 7B, cardiac muscle, beta. MYH7B has LocusID: 57644, and is located at chromosome 20q11.21.

[0366] CPS 211 corresponds to IL1B which encodes interleukin 1, beta. The gene has LocusID: 3553, and is located on chromosome 2 with reported cytogenetic location 2q14. Interleukin-1 beta may initiate and amplify the immune and inflammatory responses.

[0367] CPS 212 corresponds to STX1A which encodes syntaxin 1A (brain). The gene has LocusID: 6804, and is located on chromosome 7 with reported cytogenetic location 7q11.23. Syntaxin 1A (brain) may be involved in intracellular transport and neurotransmitter release

[0368] CPS 213 corresponds to ATPASEP (ATP9B) which encodes ATPase type IV, phospholipid transporting (P-type)(putative) (ATPase, Class II, type 9B). The gene has LocusID: 11071, and is located on chromosome 18 with reported cytogenetic location 18q23.

[0369] CPS 214 corresponds to CR1 which encodes complement component (3b/4b) receptor 1, including Knops blood group system. The gene has LocusID: 1378, and is located on chromosome 1 with reported cytogenetic location 1q32. The gene comprises 2769865 to 2857756 nucleotides of chromosome 1. This gene encodes a membrane glycoprotein found on peripheral blood cells, glomerular podocytes, and follicular dendritic cells. The protein encoded by the gene is a receptor for complement components C3b and C4b and regulates the activity of the complement cascade. Variation in the encoded protein is the basis of the Knops blood group system. The two common alleles, F and S, differ by 8 exons and are thought to be the result of an unequal crossover event. A secreted form of the encoded protein present in plasma has been described, but its full length nature has not been determined. The encoded protein has short consensus repeats (SCRs).

[0370] CPS 214 also aligns with CR1L with about 93% sequence identity. CR1L encodes complement component (3b/4b) receptor 1-like. It has LocusID: 1379, and is located at chromosome 1q32.1.

[0371] CPS 215 corresponds to DKFZP586M1523 which encodes DKFZP586M1523 protein. The gene has LocusID: 25941, and is located on chromosome 18 with reported cytogenetic location 18q12.1.

[0372] CPS 215 also aligns with LOC201347 with over 99% sequence identity. LOC201347 is located in an intron of BRUNOL4 which encodes bruno-like 4, RNA

binding protein (*Drosophila*). BRUNOL4 has LocusID: 56853, and is located on chromosome 18 with reported cytogenetic location 18q12.

[0373] CPS 216 corresponds to KRT1 which encodes keratin 1 (epidermolytic hyperkeratosis). The gene has LocusID: 3848, and is located on chromosome 12 with reported cytogenetic location 12q12-q13. The protein encoded by this gene is a member of the keratin gene family. The type II cytokeratins include basic or neutral proteins which are arranged in pairs of heterotypic keratin chains coexpressed during differentiation of simple and stratified epithelial tissues. The type II cytokeratin encoded by KRT1 can be expressed in the spinous and granular layers of the epidermis with family member KRT10. Mutations in KRT1 and KRT10 genes may be associated with bullous congenital ichthyosiform erythroderma. The type II cytokeratins are clustered in a region of chromosome 12q12-q13.

[0374] Nucleotides 4076 to 4275 of SEQ ID NO: 203 (M98776) have 87% sequence identity with KRT2A. KRT2A encodes keratin 2A (epidermal ichthyosis bullosa of Siemens). The gene has LocusID: 3849, and is located on chromosome 12 with reported cytogenetic location 12q11-q13. KRT2A gene is a member of the keratin gene family. The protein encoded by KRT2A gene is expressed in the upper spinous layer of epidermal keratinocytes. Mutations in this gene may be associated with bullous congenital ichthyosiform erythroderma. Keratin 2A is an intermediate filament component that may have a role in terminal cornification of epidermal keratinocytes. Nucleotides 3203 to 3246 of SEQ ID NO: 203 have 93% sequence identity with an intron sequence of LOC221618 which is located at chromosome 6p21.32.

[0375] CPS 217 corresponds to UNK_AF070571 (EXT1). CPS 217 aligns to the 3' untranslated region of EXT1. EXT1 encodes exostoses (multiple) 1, and has LocusID: 2131 with reported cytogenetic location 8q24.11-q24.13. Exostoses (multiple) 1 (EXT1) is an ER-resident type II transmembrane glycosyltransferase involved in the chain elongation step of heparan sulfate biosynthesis. It is involved in hereditary multiple exostoses, a disorder characterized by cartilaginous excrescences near the ends of the diaphyses of the bones of the extremities.

[0376] CPS 218 corresponds to PPP3CB which encodes protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta). The gene has LocusID: 5532, and is located on chromosome 10 with reported cytogenetic location 10q21-q22. The product encoded by the gene, which is also known as catalytic subunit of calmodulin

regulated protein phosphatase 3; may regulate activity of transcription factors involved in signal transduction and growth control.

[0377] CPS 219 corresponds to QSCN6 which encodes quiescin Q6. The gene has LocusID: 5768, and is located on chromosome 1 with reported cytogenetic location 1q24. The protein encoded by the gene contains domains of thioredoxin and ERV1, members of two long-standing gene families. The expression of QSCN6 gene is induced when fibroblasts begin to exit the proliferative cycle and enter quiescence, suggesting that QSCN6 gene may play a role in growth regulation. Quiescin Q6 has similarity to thioredoxins and *S. cerevisiae* Erv1p.

[0378] CPS 220 corresponds to PRF1 which encodes perforin 1 (pore forming protein). The gene has LocusID: 5551, and is located on chromosome 10 with reported cytogenetic location 10q22. Perforin 1 is a cytolytic, channel-forming protein, and may play a role in clearing virally infected host cells and tumor cells. CPS 220 is located in the 3' untranslated region of the gene.

[0379] Affymetrix annotation suggests that CPS 221 corresponds to FCGR3B. FCGR3B encodes Fc fragment of IgG, low affinity IIIb, receptor for (CD16). The gene has LocusID: 2215, and is located at chromosome 1q23.

[0380] Blast search against the Entrez human genome database shows that CPS 221 also aligns with FCGR3A with over 97% sequence identity. FCGR3A encodes Fc fragment of IgG, low affinity IIIa, receptor for (CD16). FCGR3A has LocusID: 2214, and is located on chromosome 1 with reported cytogenetic location 1q23. FCGR3A gene product is a Type III Fc gamma receptor. It can associate with zeta chain of the T-cell receptor complex (CD3Z), and is a member of the immunoglobulin superfamily. FCGR3B gene is located 3' to FCGR3A gene on chromosome 1.

[0381] CPS 222 corresponds to PTGS2 which encodes prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase). The gene has LocusID: 5743, and is located on chromosome 1 with reported cytogenetic location 1q25.2-q25.3. Prostaglandin-endoperoxide synthase (PTGS), also known as cyclooxygenase, is a key enzyme in prostaglandin biosynthesis, and acts both as a dioxygenase and as a peroxidase. There are two isozymes of PTGS: a constitutive PTGS1 and an inducible PTGS2. The two isoforms differ in their regulation of expression and tissue distribution. PTGS2 gene encodes PTGS2 protein, which shows 86-89% amino acid sequence identity with mouse, rat, sheep, bovine, horse and rabbit PTGS2 proteins. Human PTGS2 gene appears to be

expressed in a limited number of cell types and regulated by specific stimulatory events, suggesting that it may be responsible for the prostanoid biosynthesis involved in inflammation and mitogenesis. The expression of PTGS2 gene may be deregulated in epithelial tumors. PTGS2 protein may regulate angiogenesis and cell migration, and catalyze the rate-limiting step in the formation of inflammatory prostaglandins.

[0382] CPS 223 corresponds to OPHN1 which encodes oligophrenin 1. The gene has LocusID: 4983, and is located on chromosome X with reported cytogenetic location Xq12. Oligophrenin 1 has at least 25 exons and may encode a Rho-GTPase-activating protein. The Rho proteins are important mediators of intracellular signal transduction which affects cell migration and cell morphogenesis. Mutations in OPHN1 gene may be responsible for non-specific X-linked mental retardation. Nucleotides 2971 to 3363 of SEQ ID NO: 210 (AJ001189) have 84% sequence identity with an intron sequence of putative gene LOC200861 which is located at chromosome 3p24.1.

[0383] CPS 224 corresponds to VSNL1 which encodes visinin-like 1. The gene has LocusID: 7447, and is located on chromosome 2 with reported cytogenetic location 2p24.3. Visinin-like protein 1 may bind calcium. The protein is similar to rat Vsnl1.

[0384] CPS 225 corresponds to FECH which encodes ferrochelatase (protoporphyrin). The gene has LocusID: 2235, and is located on chromosome 18 with reported cytogenetic location 18q21.3. Ferrochelatase is localized to the mitochondrion where it catalyzes the insertion of ferrous form of iron into protoporphyrin IX in the heme synthesis pathway. Defects in ferrochelatase are associated with protoporphyria. CPS 225 is located in the 3' untranslated region of the gene.

[0385] SEQ ID NO: 282 (D00726) also aligns to FECH with over 97% sequence identity, and can be used to design probes for detecting the expression level of FECH. Nucleotides 167 to 1972 of SEQ ID NO: 282 have 82-84% sequence identity with LOC205467. LOC205467 is a putative gene, and located on chromosome 3 with reported cytogenetic location 3p22.1.

[0386] CPS 226 corresponds to KIAA0483 which encodes KIAA0483 protein. The gene has LocusID: 23219, and is located on chromosome 1 with reported cytogenetic location 1q41. CPS 227 corresponds to HK3 which encodes hexokinase 3 (white cell). The gene has LocusID: 3101, and is located on chromosome 5 with reported cytogenetic location 5q35.2. Hexokinases phosphorylate glucose to produce glucose-6-phosphate, thus committing glucose to the glycolytic pathway. HK3 gene encodes

hexokinase 3 which is similar to hexokinases 1 and 2. Hexokinase 3 is an allosteric enzyme and can be inhibited by its product glucose-6-phosphate.

[0387] CPS 228 corresponds to MS4A3 which encodes membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific). The gene has LocusID: 932, and is located on chromosome 11 with reported cytogenetic location 11q12-q13.1. The gene product has low similarity to CD20 and the beta subunit of FCER1B. It contains four predicted membrane-spanning domains, and may play a role in signal transduction.

[0388] CPS 229 corresponds to SCYA20 which encodes small inducible cytokine subfamily A (Cys-Cys), member 20. The gene has LocusID: 6364, and is located on chromosome 2 with reported cytogenetic location 2q33-q37. The gene product Cytokine A20 (exodus) is a chemotactic factor for lymphocytes, but not a chemotactic factor for monocytes.

[0389] CPS 230 corresponds to C1QR1 which encodes complement component 1, q subcomponent, receptor 1. The gene has LocusID: 22918, and is located on chromosome 20 with reported cytogenetic location 20p11.21. This gene encodes a type I membrane protein. The encoded protein acts as a receptor for complement protein C1q, mannose-binding lectin, and pulmonary surfactant protein A. The protein is a functional receptor involved in ligand-mediated enhancement of phagocytosis. It may play a role in phagocytic destruction of pathogens and immune complexes.

[0390] CPS 230 also aligns with a chromosomal region near putative gene LOC200421 with about 99% sequence identity. LOC200421 has reported cytogenetic location 2p12.

[0391] CPS 231 corresponds to POU1F1 which encodes POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1). The gene has LocusID: 5449, and is located on chromosome 3 with reported cytogenetic location 3p11. The gene product, also known as POU homeodomain transcription factor 1, may regulate PRL, GH and TSH genes.

[0392] CPS 232 corresponds to TKTL1 which encodes transketolase-like 1. The gene has LocusID: 8277, and is located on chromosome X with reported cytogenetic location Xq28. Transketolase 1 is a thiamine pyrophosphate-dependent enzyme in the pentose phosphate pathway.

[0393] CPS 234 corresponds to CCNT2 which encodes cyclin T2. The gene has LocusID: 905, and is located on chromosome 2 with reported cytogenetic location 2q14.3. The protein encoded by this gene belongs to a highly conserved cyclin family, whose

members are characterized by a dramatic periodicity in protein abundance through the cell cycle. Cyclins function as regulators of CDK kinases. Different cyclins exhibit distinct expression and degradation patterns which contribute to the temporal coordination of each mitotic event. Cyclin T2 and its kinase partner CDK9 were found to be subunits of the transcription elongation factor p-TEFb. The p-TEFb complex containing cyclin T2 was reported to interact with, and act as a negative regulator of human immunodeficiency virus type 1 (HIV-1) Tat protein. At least two alternatively spliced transcript variants, which encode distinct isoforms, have been described.

[0394] Nucleotides 261 to 723 and 936 to 1349 of SEQ ID NO: 220 (AF048732) have about 88% sequence identity to a chromosomal region on chromosome 1.

[0395] CPS 235 corresponds to ATP6V1H which encodes ATPase, H⁺ transporting, lysosomal 50/57kD V1 subunit H. The gene has LocusID: 51606, and is located on chromosome 8 with reported cytogenetic location 8p22-q22.3. The polypeptide encoded by the gene is also known as CGI-11 protein [H.sapiens]. An intron of ATP6V1H gene includes RGS20 gene. RGS20 encodes regulator of G-protein signalling 20, and has LocusID: 8601.

[0396] CPS 236 corresponds to FN1 which encodes fibronectin 1. The gene has LocusID: 2335, and is located on chromosome 2 with reported cytogenetic location 2q34. Fibronectin is a glycoprotein present in a soluble dimeric form in plasma, and in a dimeric or multimeric form at the cell surface and in extracellular matrix. Fibronectin is involved in cell adhesion and migration processes including embryogenesis, wound healing, blood coagulation, host defense, and metastasis. FN1 gene has three regions subject to alternative splicing, with the potential to produce 20 different transcript variants.

[0397] CPS 237 corresponds to UNK_J04178 which is located in an intron of HEXA. HEXA encodes hexosaminidase A (alpha polypeptide). HEXA has LocusID: 3073, and is located on chromosome 15 with reported cytogenetic location 15q23-q24. Hexosaminidase A is the alpha subunit of the lysosomal enzyme beta-hexosaminidase which, together with the cofactor GM2 activator protein, catalyzes the degradation of the ganglioside GM2, and other molecules containing terminal N-acetyl hexosamines. Beta-hexosaminidase is composed of two subunits, alpha and beta, which are encoded by separate genes. Both beta-hexosaminidase alpha and beta subunits are members of family 20 of glycosyl hydrolases. Mutations in the alpha or beta subunit genes may lead to an accumulation of GM2 ganglioside in neurons and neurodegenerative disorders termed the

GM2 gangliosidoses. Alpha subunit gene mutations may lead to Tay-Sachs disease (GM2-gangliosidosis type I). The chromosomal region that aligns to CPS 237 is located in an intron of HEXA.

[0398] CPS 237 also aligns with LOC145709 which is a hypothetical gene supported by J04178. LOC145709 has reported cytogenetic location 15q22.32.

[0399] CPS 239 corresponds to NR2C1 which encodes nuclear receptor subfamily 2, group C, member 1. The gene has LocusID: 7181, and is located on chromosome 12 with reported cytogenetic location 12q21.32-q21.33. The gene product can exist in multiple isoforms with different ligand-binding domains.

[0400] CPS 240 corresponds to RASSF2 (KIAA0168) which encodes Ras association (RalGDS/AF-6) domain family 2. The gene has LocusID: 9770, and is located on chromosome 20 with reported cytogenetic location 20pter-p12.1. The alternative name for this gene product is KIAA0168 protein.

[0401] CPS 241 corresponds to IL6 which encodes interleukin 6 (interferon, beta 2). The gene has LocusID: 3569, and is located on chromosome 7 with reported cytogenetic location 7p21. Interleukin 6 (interferon-beta 2) may induce the maturation of B cells into immunoglobulin-secreting cells.

[0402] CPS 242 corresponds to KIAA0372 which encodes KIAA0372 gene product. The gene has LocusID: 9652, and is located on chromosome 5 with reported cytogenetic location 5q21.1-q21.2.

[0403] CPS 243 corresponds to CYP4F2 which encodes cytochrome P450, subfamily IVF, polypeptide 2. The gene has LocusID: 8529, and is located on chromosome 19 with reported cytogenetic location 19pter-p13.11. This gene encodes a member of the cytochrome P450 superfamily of enzymes. The cytochrome P450 proteins are monooxygenases which catalyze many reactions involved in drug metabolism and synthesis of cholesterol, steroids and other lipids. The cytochrome P450 proteins localize to the endoplasmic reticulum. They may start the process of inactivating and degrading leukotriene B4, a potent mediator of inflammation. CYP4F2 gene is part of a cluster of cytochrome P450 genes on chromosome 19. Another member of this family, CYP4F11, is approximately 16 kb away.

[0404] CPS 243 also aligns with CYP4F3 with about 97% sequence identity. CYP4F3 encodes cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase). It has LocusID: 4051, and is located on chromosome 19 with reported

cytogenetic location 19p13.2. CYP4F3 encodes a member of the cytochrome P450 superfamily of enzymes. This gene is also part of a cluster of cytochrome P450 genes on chromosome 19. Another member of this family, CYP4F8, is approximately 18 kb away. CYP4F3 gene product may convert leukotriene B4 into the less active 20-hydroxy-leukotriene B4.

[0405] Various fragments in nucleotides 253 to 1639 of U02388 (SEQ ID NO: 228) align to various genes with about 83-93% sequence identity. These genes include LOC126538, LOC126537, LOC126407, CYP4F12, and CYP4F8. LOC126538 and LOC126537 encode proteins similar to cytochrome P450, subfamily IVF, polypeptide 2 (leukotriene B4 omega-hydroxylase) (leukotriene-B4 20-monooxygenase). Both genes are located at chromosome 19p13.12. LOC126407 encodes a protein similar to cytochrome P450, and is located on chromosome 19. CYP4F12 encodes cytochrome P450, subfamily IVF, polypeptide 12. CYP4F12 has LocusID: 66002. CYP4F8 encodes cytochrome P450, subfamily IVF, polypeptide 8, and has LocusID: 11283.

[0406] Nucleotides 446 to 1457 of SEQ ID NO: 228 (U02388) also align with a chromosomal region between the coding sequences of LOC222275 and CYP4F11. LOC222275 encodes a protein similar to mitochondrial RNA polymerase, and has reported cytogenetic location 19p13.12. CYP4F11 encodes cytochrome P450, subfamily IVF, polypeptide 11, and has LocusID: 57834. CYP4F11 has reported cytogenetic location 19p13.1.

[0407] CPS 244 corresponds to STIP1 which encodes stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein). The gene has LocusID: 10963, and is located on chromosome 11 with reported cytogenetic location 11q13.

[0408] Nucleotides 1 to 1086 of SEQ ID NO: 229 (M86752) have 100% sequence identity with STIP1. STIP1 encodes stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein). The gene has LocusID: 10963, and is located on chromosome 11 with reported cytogenetic location 11q13. The gene product is similar to *S. cerevisiae* Stip1, and has TPR repeats. The sequence alignment between nucleotides 1 to 1086 of M86752 and STIP1 is located in an intron of putative gene LRP16. LRP16 encodes LRP16 protein, and has LocusID: 28992. LRP16 has reported cytogenetic location 11q11. LRP16 gene product contains a region having low similarity to the H2A histone family.

[0409] Nucleotides 69 to 1086 of SEQ ID NO: 229 have over 99% sequence identity with a chromosomal region between the coding sequences of NAALADASEL and

LOC220489. NAALADASEL encodes N-acetylated alpha-linked acidic dipeptidase-like (ILEAL DIPEPTIDYLPEPTIDASE), and has LocusID: 10004. LOC220489 encodes a protein similar to stress-induced phosphoprotein 1.

[0410] Moreover, CPS 244 aligns with LOC170030 and a region near LOC121392 with 85-93% sequence identity. LOC170030 encodes a protein similar to transformation-sensitive protein IEF SSP 3521 (human). It is located at chromosome Xq21.1. LOC121392 encodes a protein similar to keratin complex 2, gene 6g. It is located at chromosome 12q12.

[0411] CPS 245 corresponds to SERPINH2 (CBP2) which encodes serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2. The gene has LocusID: 872, and is located on chromosome 11 with reported cytogenetic location 11q13.5. The gene product is also known as collagen-binding protein 2 or colligen 2. It is a collagen-binding protein that acts as a heat shock protein.

[0412] CPS 245 also aligns with LOC158172 with about 91% sequence identity. LOC158172 encodes a protein similar to collagen-binding protein 2 precursor (colligin 2) (Rheumatoid arthritis related antigen RA-A47). LOC158172 is located at chromosome 9p11.2.

[0413] CPS 247 corresponds to NCF1 which encodes neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1). The gene has LocusID: 4687, and is located on chromosome 7 with reported cytogenetic location 7q11.23. NCF1 encodes neutrophil cytosolic factor 1, the 47-kilodalton cytosolic subunit of the multi-protein complex known as NADPH oxidase found in neutrophils. This oxidase produces a burst of superoxide which is delivered to the lumen of the neutrophil phagosome. Mutations in NCF1, as well as in other NADPH oxidase subunits, may result in chronic granulomatous disease.

[0414] CPS 247 also aligns with LOC220830 with over 95% sequence identity. LOC220830 encodes a protein similar to neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1). LOC220830 is located on chromosome 7 with reported cytogenetic location 7p13.

[0415] Affymetrix annotation suggests that CPS 248 corresponds to CHN2. Blast search against the Entrez human genome database shows that CPS 248 also aligns to the 3' untranslated region of LOC222172 with 99% sequence identity. LOC222172 encodes Beta-chimaerin (Beta-chimerin). The gene is located on chromosome 7 with reported cytogenetic location 7p21.1-p15.3.

[0416] Nucleotides 456 to 2446 of SEQ ID NO: 284 (U07223) align with LOC222172 with over 97% sequence identity. Nucleotides 4 to 473 of SEQ ID NO: 284 (U07223) have 97% sequence identity with GFAP. GFAP encodes glial fibrillary acidic protein. It has LocusID: 2670, and is located on chromosome 17 with reported cytogenetic location 17q21. Glial fibrillary acidic protein is an intermediate filament protein.

[0417] CPS 249 corresponds to ABL1 which encodes v-abl Abelson murine leukemia viral oncogene homolog 1. The gene has LocusID: 25, and is located on chromosome 9 with reported cytogenetic location 9q34.1. The ABL1 protooncogene encodes a cytoplasmic and nuclear protein tyrosine kinase that has been implicated in processes of cell differentiation, cell division, cell adhesion, and stress response. Activity of ABL1 protein is negatively regulated by its SH3 domain, and deletion of the SH3 domain turns ABL1 into an oncogene. The t(9;22) translocation results in the head-to-tail fusion of the BCR (MIM:151410) and ABL1 genes present in many cases of chronic myelogenous leukemia. The DNA-binding activity of the ubiquitously expressed ABL1 tyrosine kinase is regulated by CDC2-mediated phosphorylation, suggesting a cell cycle function for ABL1. The ABL1 gene can be expressed as a 6- or 7-kb mRNA transcript, with alternatively spliced first exons spliced to the common exons 2-11.

[0418] CPS 250 corresponds to FLOT1 which encodes flotillin 1. The gene has LocusID: 10211, and is located on chromosome 6 with reported cytogenetic location 6p21.3. Caveolae are small domains on the inner cell membrane involved in vesicular trafficking and signal transduction. FLOT1 encodes a caveolae-associated, integral membrane protein. The function of flotillin 1 has not been determined. Flotillin 1 is similar to murine flotillin (Mm.2931).

[0419] CPS 250 also aligns to an intron sequence of LOC203011 with about 91% sequence identity. LOC203011 is located at chromosome 8q23.3.

[0420] CPS 251 corresponds to REV3L which encodes REV3-like, catalytic subunit of DNA polymerase zeta (yeast). The gene has LocusID: 5980, and is located on chromosome 6 with reported cytogenetic location 6q21. Catalytic subunit of DNA polymerase zeta acts in translation replication, and may be involved in mutagenesis.

[0421] Affymetrix annotation suggests that CPS 252 corresponds to MUC3 which encodes mucin 3, intestinal. The gene has LocusID: 4584, and is located on chromosome 7 with reported cytogenetic location 7q22.

[0422] CPS 253 corresponds to SMARCA4 which encodes SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4. The gene has LocusID: 6597, and is located on chromosome 19 with reported cytogenetic location 19p13.2. The protein encoded by this gene is a member of the SWI/SNF family of proteins and is similar to the brahma protein of Drosophila. Members of this family have helicase and ATPase activities and are thought to regulate transcription of certain genes by altering the chromatin structure around those genes. The encoded protein is part of the large ATP-dependent chromatin remodeling complex SNF/SWI, which is required for transcriptional activation of genes normally repressed by chromatin. In addition, the encoded protein can bind BRCA1, as well as regulate the expression of the tumorigenic protein CD44. Alternatively spliced transcripts have been found for this gene.

[0423] Nucleotides 2063 to 2094 of SEQ ID NO: 238 (U29175) have 100% sequence identity with various regions in the human genome. These regions include LOC203511, which is located at chromosome Xp22.31, and a chromosomal region near LOC200164 on chromosome 1.

[0424] CPS 254 corresponds to LOC92684 which encodes hypothetical gene supported by AF035314. The gene is located on chromosome 20 with reported cytogenetic location 20p11.21. The sequence alignment between CPS 254 and LOC92684 is located in an intron of C20orf19. C20orf19 refers to chromosome 20 open reading frame 19. It has LocusID: 55857, and is reportedly located at chromosome 20pter-q11.23.

[0425] CPS 255 corresponds to EEF1A2 which encodes eukaryotic translation elongation factor 1 alpha 2. The gene has LocusID: 1917, and is located on chromosome 20 with reported cytogenetic location 20q13.3. The gene product has a guanine nucleotide-binding site, and may be involved in the binding of aminoacyl-tRNA to the ribosome during peptide synthesis.

[0426] CPS 256 corresponds to BRF2 (ZFP36L2) which encodes zinc finger protein 36, C3H type-like 2. The gene has LocusID: 678, and is located on chromosome 2 with reported cytogenetic location 2p22.3-p21. This gene is a member of the TIS11 family of early response genes. Family members are induced by various agonists such as the phorbol ester TPA and the polypeptide mitogen EGF. The protein encoded by this gene contains a distinguishing putative zinc finger domain with a repeating cys-his motif. The encoded protein is a putative nuclear transcription factor, and may function in regulating the

response to growth factors. The sequence alignment between CPS 256 and BRF2 overlaps LOC151103 and LOC165204.

[0427] Nucleotides 3862 to 4187 and 4238 to 4907 of SEQ ID NO: 286 have 84-86% sequence identity to a chromosomal region near LOC143974. LOC143974 is located at chromosome 11p14.1. Nucleotides 5004 to 5497 of SEQ ID NO: 286 align to an intron sequence of KIAA1301 with 82% sequence identity. KIAA1301 encodes KIAA1301 protein, and is located at chromosome 2q33.1.

[0428] CPS 257 corresponds to SNRPG which encodes small nuclear ribonucleoprotein polypeptide G. The gene has LocusID: 6637, and is located on chromosome 2 with reported cytogenetic location 2p12. The gene product is also known as spliceosomal snRNA-associated Sm core protein G, and may be involved in the biogenesis of the snRNPs.

[0429] CPS 257, or fragments thereof, also aligns to various regions or genes with about 95-96% sequence identity. These regions or genes include a chromosomal region between LOC162681 and LOC125307, an intron sequence of RGS19IP1, an intron sequence of FLJ10748, a chromosomal region near SKD3, POLE2, and an intron sequence of OPTN. Both LOC162681 and LOC125307 have reported cytogenetic location 18q21.2. RGS19IP1 encodes regulator of G-protein signalling 19 interacting protein 1, and has LocusID: 10755. RGS19IP1 is located on chromosome 19 with reported cytogenetic location 19p13.1. FLJ10748 encodes hypothetical protein FLJ10748, and is reportedly located at chromosome 1q31.2. SKD3 encodes suppressor of potassium transport defect 3. It has LocusID: 81570 and reported cytogenetic location 11q13.3. POLE2 encodes polymerase (DNA directed), epsilon 2 (p59 subunit), and has LocusID: 5427. It is located at chromosome 14q21-q22. OPTN encodes optineurin, and has LocusID: 10133. OPTN is located at chromosome 10p12.33.

[0430] In addition, fragments of CPS 257 align to various regions or genes with about 85-92% sequence identity. These regions or genes include a chromosomal region near LOC164917, a region located 5' to ABCA5, an intron sequence of KIAA1170, and chromosomal regions near SPG3A, LOC201203, LOC205322, LOC203775 and ERG, respectively. LOC164917 is located at chromosome 2q12.2. ABCA5 encodes ATP-binding cassette, sub-family A (ABC1), member 5. ABCA5 has LocusID: 23461, and is located at chromosome 17q24.3. KIAA1170 encodes KIAA1170 protein, and is located at chromosome 7q31.1. SPG3A encodes spastic paraplegia 3A (autosomal dominant).

SPG3A has LocusID: 51062, and is located at chromosome 14q21.3. LOC201203, LOC205322, LOC203775 and ERG are located at chromosome 17q22, 2p23.3, 10q26.2 and 21q22.3, respectively. LOC203775 encodes a protein similar to high mobility group protein 4 (HMG-4) (high mobility group protein 2a) (HMG-2a). ERG encodes v-ets erythroblastosis virus E26 oncogene like (avian), and has LocusID: 2078.

[0431] CPS 258 corresponds to NUMA1 which encodes nuclear mitotic apparatus protein 1. The gene has LocusID: 4926, and is located on chromosome 11 with reported cytogenetic location 11q13. The gene product is a structural component of the nucleus. It contains a predicted coiled-coil domain, and is predicted to have a role in nuclear reassembly in late mitosis.

[0432] CPS 259 corresponds to AKR1B1 which encodes aldo-keto reductase family 1, member B1 (aldose reductase). The gene has LocusID: 231, and is located on chromosome 7 with reported cytogenetic location 7q35. The gene product is also known as aldo-keto reductase 1B1 (aldose reductase, aldehyde dehydrogenase). It can reduce glucose and other carbonyl-containing substrates. The gene product is a member of the NADPH-dependent aldo-keto reductase superfamily.

[0433] Fragments of SEQ ID NO: 289 align to other genes or regions with about 83-92% sequence identity. These genes or regions include LOC126242, LOC163862, LOC131710, LOC145401, LOC170139, LOC125836, and a chromosomal region near LOC220082. LOC126242 encodes a protein similar to aldose reductase (AR) (aldehyde reductase), and is located at chromosome 19q13.12. LOC163862 also encodes a protein similar to aldose reductase. It is located at chromosome 1q41. LOC131710 and LOC125836 encodes proteins similar to aldose reductase (E.C.1.1.1.21) (Mutant With Tyr 48 Replaced By His (Y48h) Complexed With Nadp+ And Citrate), and are located at chromosome 3p13 and 18p11.21, respectively. LOC145401 encodes a protein similar to aldo-keto reductase family 1, member B1 (aldose reductase). LOC145401 is located at chromosome 14q22.3. LOC170139 is located at chromosome Xq23, and encodes a protein similar to aldose reductase (AR) (aldehyde reductase). LOC220082 is located at chromosome 13q14.11.

[0434] CPS 260 corresponds to SMARCE1 which encodes SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1. The gene has LocusID: 6605, and is located on chromosome 17 with reported cytogenetic location 17q21.1. The protein encoded by this gene is part of the large ATP-dependent chromatin

remodeling complex SWI/SNF, which is required for transcriptional activation of genes normally repressed by chromatin. The encoded protein, either alone or when in the SWI/SNF complex, can bind to 4-way junction DNA, which is thought to mimic the topology of DNA as it enters or exits the nucleosome. The encoded protein contains a DNA-binding HMG domain, but disruption of this domain does not abolish the DNA-binding or nucleosome-displacement activities of the SWI/SNF complex. SNF/SWI complex is associated with the nuclear matrix and implicated in regulation of transcription by affecting chromatin structure.

[0435] SEQ ID NO: 290 aligns to SMARCE1 with over 98% sequence identity and therefore, can be used to prepare probes directed to SMARCE1. Nucleotides 10 to 1377 of SEQ ID NO: 290 (AF035262) also show about 90-94% sequence identity with LOC160863, LOC145357 and LOC134699. All of these three putative genes encode proteins similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1. LOC160863, LOC145357 and LOC134699 are located at chromosome 13q14.11, 14q11.1 and 6q16.1, respectively.

[0436] CPS 261 corresponds to KIAA0669 which encodes KIAA0669 gene product. The gene has LocusID: 9819, and is located on chromosome 3 with reported cytogenetic location 3q25.1. Affymetrix annotation suggests that CPS 262 corresponds to MSF which encodes MLL septin-like fusion. The gene has LocusID: 10801, and is located on chromosome 17 with reported cytogenetic location 17q25.

[0437] SEQ ID NO: 292 aligns to a chromosomal region on chromosome 17 with over 99% sequence identity. The region includes LOC204508, FLJ12190, LOC204512 and LOC197453. All of these genes have reported cytogenetic location 17q25.3. FLJ12190 has LocusID: 80141. LOC197453 encodes a protein similar to hypothetical protein SBBI23.

[0438] CPS 263 corresponds to PTMA which encodes prothymosin, alpha (gene sequence 28). The gene has LocusID: 5757, and is located on chromosome 2 with reported cytogenetic location 2q35-q36. Prothymosin alpha may be associated with cell proliferation.

[0439] Nucleotides 43 to 1200 of SEQ ID NO: 293 also align to LOC220771 with 98% sequence identity. LOC220771 encodes prothymosin alpha, and is reportedly located at chromosome 5q23.2. In addition, CPS 263, or fragments thereof, align with LOC145123, LOC220508, a chromosomal region between PZP and DDX12, and an intron sequence of TRIP11 with about 94-95% sequence identity. LOC145123 is located at chromosome

13q22.3. LOC220508 encodes prothymosin alpha, and is located at chromosome 12p12.3. PZP encodes pregnancy-zone protein, and has LocusID: 5858. It is located at chromosome 12p13-p12.2. DDX12 encodes DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12 (CHL1-like helicase homolog, *S. cerevisiae*), and has LocusID: 1664. DDX12 is located at chromosome 12p13. TRIP11 encode thyroid hormone receptor interactor 11, and has LocusID: 9321. TRIP11 is located at chromosome 14q31-q32. CPS 263, or fragments thereof, also aligns to other regions in the human genome with 90-95% sequence identity.

[0440] CPS 264 corresponds to KIAA0410 which encodes KIAA0410 gene product. The gene has LocusID: 9818, and is located on chromosome 13 with reported cytogenetic location 13q12.12.

[0441] CPS 265 corresponds to PSMD3 which encodes proteasome (prosome, macropain) 26S subunit, non-ATPase, 3. The gene has LocusID: 5709, and is located on chromosome 17 with reported cytogenetic location 17q12.

[0442] CPS 266 corresponds to C1QBP which encodes complement component 1, q subcomponent binding protein. The gene has LocusID: 708, and is located on chromosome 17 with reported cytogenetic location 17p13.3. The human complement subcomponent C1q associates with C1r and C1s to yield the first component of the serum complement system. The protein encoded by C1QBP gene is known to bind to the globular heads of C1q molecules and inhibit C1 activation. This protein has also been identified as the p32 subunit of pre-mRNA splicing factor SF2, as well as a hyaluronic acid-binding protein.

[0443] Nucleotides 58 to 1071 and 107 to 1037 of SEQ ID NO: 296 align to C1QBPP and an intron sequence of RYR3 with 79-84% sequence identity. C1QBPP encodes complement component 1, q subcomponent binding protein, pseudogene. It has LocusID: 54098, and is located at chromosome 21q21.1. RYR3 encodes ryanodine receptor 3. RYR3 has LocusID: 6263, and is located at chromosome 15q14-q15.

[0444] In addition, nucleotides 1070 to 1227 of SEQ ID NO: 296 align to LOC221903 with 100% sequence identity. LOC221903 is a hypothetical gene supported by AF000974, BC004999, AF000974, BC021540, BC004249, AJ001902, AF025437, L40374, BC004999, AF025437, AK056773, BC002680, AK056773, BC004999, and BC002680. The gene is located at chromosome 7q11.1.

[0445] CPS 267 corresponds to OSR1 which encodes oxidative-stress responsive 1. The gene has LocusID: 9943, and is located on chromosome 3 with reported cytogenetic location 3p22-p21.3. Oxidative-stress responsive 1 gene has at least 18 exons and is located

in the vicinity of three others genes - GOLGA4, ITGA9 and HYA22. These four genes are considered to be candidate tumor suppressors. Oxidative-stress responsive 1 protein has similarity to human Ste20/oxidant stress response kinase-1 and is thought to be involved in the response to oxidative stress. Oxidative-stress responsive 1 protein is a putative member of SOK (Ste20/oxidant stress response kinase) family, and can be activated by oxidative stress.

[0446] CPS 268 corresponds to CD44 which encodes CD44 antigen (homing function and Indian blood group system). The gene has LocusID: 960, and is located on chromosome 11 with reported cytogenetic location 11p13.

[0447] CPS 269 corresponds to CRADD which encodes CASP2 and RIPK1 domain containing adaptor with death domain. The gene has LocusID: 8738, and is located on chromosome 12 with reported cytogenetic location 12q21.33-q23.1. The gene product is an apoptotic adaptor molecule, and may function to couple CASP2 to the FasL/TNF receptor-interacting protein RIP.

[0448] CPS 270 corresponds to CCRL2 which encodes chemokine (C-C motif) receptor-like 2. The gene has LocusID: 9034, and is located on chromosome 3 with reported cytogenetic location 3p21. This gene encodes a chemokine receptor-like protein, which is predicted to be a seven transmembrane protein and most closely related to CCR1. Chemokines and their receptors are believed to be critical for the recruitment of effector immune cells to the site of inflammation. CCRL2 gene is expressed at high levels in primary neutrophils and primary monocytes, and is further upregulated on neutrophil activation and during monocyte to macrophage differentiation. CCRL2 gene is mapped to the region where the chemokine receptor gene cluster is located. The gene product is a member of the G protein-coupled receptor family.

[0449] CPS 271 corresponds to KIAA0707 (THEA) which encodes thioesterase, adipose associated. The gene has LocusID: 26027, and is located on chromosome 1 with reported cytogenetic location 1p32.2.

[0450] CPS 272 corresponds to KIAA1113 (TRIM33) which encodes tripartite motif-containing 33. The gene has LocusID: 51592, and is located on chromosome 1 with reported cytogenetic location 1p13.1. The protein encoded by this gene is thought to be a transcriptional corepressor. The encoded protein is a member of the tripartite motif family. The tripartite motif includes three zinc-binding domains, a RING, a B-box type 1 and a B-

box type 2, and a coiled-coil region. At least three alternatively spliced transcript variants for this gene have been described.

[0451] CPS 273 corresponds to a chromosomal region on chromosome 21. This region is referred to as UNK_AL050119. The region is located in an intron of TMEM1 which encodes transmembrane protein 1. TMEM1 has LocusID: 7109 with reported cytogenetic location 21q22.3. TMEM1 gene product is similar to sodium channel proteins.

[0452] CPS 274 corresponds to UNK_AF052115 (LOC151405) which is a hypothetical gene supported by AF052115. The gene has reported cytogenetic location 2q33.3. LOC151405 gene is located 3' to the polypeptide-coding sequence of ADAM23 which encodes disintegrin and metalloproteinase domain 23. ADAM23 has LocusID: 8745, and is located on chromosome 2 with reported cytogenetic location 2q33. ADAM23 gene product is a member of the ADAM protein family. Members of this family are membrane-anchored proteins structurally related to snake venom disintegrins, and have been implicated in a variety of biologic processes involving cell-cell and cell-matrix interactions, including fertilization, muscle development, and neurogenesis.

[0453] CPS 275 corresponds to MITF which encodes microphthalmia-associated transcription factor. The gene has LocusID: 4286, and is located on chromosome 3 with reported cytogenetic location 3p14.1-p12.3. MITF gene product contains both basic helix-loop-helix and leucine zipper structural features. MITF produces at least two alternate transcripts: the M-isoform expressed exclusively in melanocytes, and the A-isoform with a broader range of expression. Mutations in MITF may lead to Waardenburg syndrome.

[0454] CPS 276 corresponds to STAT3 which encodes signal transducer and activator of transcription 3 (acute-phase response factor). The gene has LocusID: 6774, and is located on chromosome 17 with reported cytogenetic location 17q21.

[0455] The protein encoded by this gene is a member of the STAT protein family. In response to cytokines and growth factors, STAT family members can be phosphorylated by the receptor associated kinases, and then form homo- or heterodimers that translocate to the cell nucleus where they act as transcription activators. The protein encoded by STAT3 gene can be activated through phosphorylation in response to various cytokines and growth factors including IFNs, EGF, IL5, IL6, HGF, LIF and BMP2. The encoded protein can mediate the expression of a variety of genes in response to cell stimuli, and thus plays a role in many cellular processes such as cell growth and apoptosis. The small GTPase Rac1 has been shown to bind and regulate the activity of this protein. PIAS3 protein is a specific

inhibitor of this protein. Two alternatively spliced transcript variants encoding distinct isoforms have been described.

[0456] In addition, nucleotides 16 to 2787 of SEQ ID NO: 315 (L29277) have at least 95% sequence identity with STAT3. Therefore, SEQ ID NO: 315 (L29277), or the complement thereof, can be used to design probes/primers for detecting the expression of STAT3. Nucleotides 217 to 1502 of SEQ ID NO: 315 (L29277) have at least 98% sequence identity with LOC254114. LOC254114 encodes a protein similar to signal transducer and activator of transcription 3 (acute-phase response factor). LOC254114 is located on chromosome 17.

[0457] CPS 277 corresponds to TPD52L2 which encodes tumor protein D52-like 2. The gene has LocusID: 7165, and is located on chromosome 20 with reported cytogenetic location 20q13.2-q13.3. The gene product is a member of the D52-like family of proteins, and may have a role in controlling cell proliferation. The gene product contains coiled-coil domains.

[0458] CPS 278 corresponds to a chromosomal region (referred to as UNK_AI732885). This chromosomal region is located in an intron of CG005 which encodes a hypothetical protein from BCRA2 region. CG005 has LocusID: 10443 with reported cytogenetic location 13q12-q13. CG005 gene product includes a region having low similarity to a region of rat 2',3'-cyclic nucleotide 3'-phosphodiesterase (Rn.31762).

[0459] CPS 279 corresponds to MAP3K8 which encodes mitogen-activated protein kinase kinase kinase 8. The gene has LocusID: 1326, and is located on chromosome 10 with reported cytogenetic location 10p11.2. This gene was identified by its oncogenic transforming activity in cells. The encoded protein is a member of the serine/threonine protein kinase family. This kinase can activate both the MAP kinase and JNK kinase pathways. This kinase was shown to activate I κ B kinases, and thus induce the nuclear production of NF- κ B. This kinase was also found to promote the production of TNF- α and IL-2 during T lymphocyte activation. Studies of a similar gene in rat suggested the direct involvement of this kinase in the proteolysis of NF- κ B1,p105 (NFKB1). MAP3K8 gene may also utilize a downstream in-frame translation start codon, and thus produce an isoform containing a shorter N-terminus. The shorter isoform has been shown to display weaker transforming activity.

[0460] CPS 280 corresponds to NSP-CL (RTN4) which encodes reticulon 4. The gene has LocusID: 57142, and is located on chromosome 2 with reported cytogenetic

location 2p14-p13. RTN4 gene overlaps LOC200512 on chromosome 2. LOC200512 encodes a protein similar to reticulon 4. LOC200512 has reported cytogenetic location 2p16.1.

[0461] CPS 281 corresponds to NRG1 which encodes neuregulin 1. The gene has LocusID: 3084, and is located at chromosome 8 with reported cytogenetic location 8p21-p12. Neuregulin 1 was originally identified as a 44-kD glycoprotein that interacts with the NEU/ERBB2 receptor tyrosine kinase to increase its phosphorylation on tyrosine residues. It is known that an extraordinary variety of different isoforms are produced from the NRG1 gene by alternative splicing. These isoforms include heregulins (HRGs), glial growth factors (GGFs) and sensory and motor neuron-derived factor (SMDF). They are tissue-specifically expressed and differ significantly in their structure. The HRG isoforms all contain immunoglobulin (Ig) and epidermal growth factor-like (EGF-like) domains. The GGF and GGF2 isoforms contain a kringle-like sequence plus Ig and EGF-like domains, and the SMDF isoform shares only the EGF-like domain with other isoforms. The receptors for all NRG1 isoforms are the ERBB family of tyrosine kinase transmembrane receptors. Through interaction with ERBB receptors, NRG1 isoforms may induce the growth and differentiation of epithelial, neuronal, glial, and other types of cells.

[0462] CPS 282 corresponds to RAB31 which encodes RAB31, member RAS oncogene family. The gene has LocusID: 11031, and is located on chromosome 18 with reported cytogenetic location 18p11.3. The gene product is a GTP-binding protein.

[0463] CPS 282 also aligns to LOC12414 and LOC200972 with 83% sequence identity. LOC124146 has reported cytogenetic location 16q11.2, and encodes a protein similar to GTP-binding protein Rab0. LOC200972 is located on chromosome 3, and also encodes a protein similar to GTP-binding protein Rab0.

[0464] CPS 283 corresponds to MEF2D which encodes MADS box transcription enhancer factor 2, polypeptide D (myocyte enhancer factor 2D). The gene has LocusID: 4209, and is located on chromosome 1 with reported cytogenetic location 1q12-q23. The gene product is a member of the MADS box family of transcription factors, and may regulate muscle-specific and mitogen-inducible genes.

[0465] CPS 285 corresponds to CXCR4 which encodes chemokine (C-X-C motif) receptor 4. The gene has LocusID: 7852, and is located on chromosome 2 with reported cytogenetic location 2q21. CXC chemokine receptor (fusin) is a G protein-coupled receptor which can mediate intracellular calcium flux.

[0466] CPS 286 corresponds to M9 which encodes muscle specific gene. The gene has LocusID: 27335, and is located on chromosome 19 with reported cytogenetic location 19q13.2.

[0467] Nucleotides 109 to 858 of SEQ ID NO: 318 have 88% sequence identity with LOC134505 which is similar to muscle specific gene. LOC134505 is located on chromosome 5 with reported cytogenetic location 5q15. Nucleotides 100 to 856 of SEQ ID NO: 318 also align to a chromosomal region on chromosome 4 with about 85% sequence identity. The chromosomal region encompasses LOC152771 which is similar to PRO1474. LOC152771 has reported cytogenetic location 4q26. In addition, nucleotides 140 to 799 of SEQ ID NO: 318 align to LOC131480 with about 84% sequence identity. LOC131480 encodes a protein similar to PRO1474, and has reported cytogenetic location 3p24.1.

[0468] CPS 287 corresponds to FAU which encodes Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30. The gene has LocusID: 2197, and is located on chromosome 11 with reported cytogenetic location 11q13. This gene is the cellular homolog of the fox sequence in the Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV). It encodes a fusion protein consisting of the ubiquitin-like protein fubi at the N terminus and ribosomal protein S30 at the C terminus. It has been proposed that the fusion protein is post-translationally processed to generate free fubi and free ribosomal protein S30. Fubi is a member of the ubiquitin family, and ribosomal protein S30 belongs to the S30E family of ribosomal proteins. Pseudogenes derived from this gene are present in the genome.

[0469] SEQ ID NO: 319 also aligns to FAUP1 with about 92% sequence identity. FAUP1 encodes FBR-MuSV-associated ubiquitously expressed (fox derived) pseudogene 1. The gene has LocusID: 140623, and is located on chromosome 18. Nucleotides 57 to 351 of SEQ ID NO: 319 have about 84% sequence identity with LOC151661. LOC151661 encodes a protein similar to ubiquitin-like/S30 ribosomal fusion protein. LOC151661 has reported cytogenetic location 3q27.2. In addition, nucleotides 454 to 490 of SEQ ID NO: 319 align to an intron sequence of RHOBTB1 with 97% sequence identity. RHOBTB1 encodes Rho-related BTB domain containing 1, and has LocusID: 9886 with reported cytogenetic location 10q22.1.

[0470] CPS 288 corresponds to RPS6 which encodes ribosomal protein S6. The gene has LocusID: 6194, and is located on chromosome 9 with reported cytogenetic location 9p21. This gene encodes a cytoplasmic ribosomal protein that is a component of

the 40S subunit in ribosome. The encoded protein belongs to the S6E family of ribosomal proteins. It is the major substrate of protein kinases in the ribosome, with subsets of five C-terminal serine residues phosphorylated by different protein kinases. It is reported that phosphorylation can be induced by a wide range of stimuli, including growth factors, tumor-promoting agents, and mitogens. Dephosphorylation occurs at growth arrest. The encoded protein may contribute to the control of cell growth and proliferation through the selective translation of particular classes of mRNA. This gene has multiple processed pseudogenes dispersed through the genome.

[0471] Fragments of SEQ ID NO: 320 align to various chromosomal regions with about 80-97% sequence identity. These chromosomal regions include, for example, LOC205865, LOC137397, LOC253482, and an intron sequence of GCDH. LOC205865 encodes a protein similar to ribosomal protein S6. The gene has reported cytogenetic location 4q21.22. LOC137397 encodes a protein similar to Rim2 protein, and is located at chromosome 8q22.3. LOC253482 encodes a protein similar to ribosomal protein S6, and is located on chromosome 9. GCDH encodes glutaryl-Coenzyme A dehydrogenase. GCDH has LocusID: 2639, and is located at chromosome 19p13.2.

[0472] CPS 289 corresponds to BAG5 which encodes BCL2-associated athanogene 5. The gene has LocusID: 9529, and is located on chromosome 14 with reported cytogenetic location 14q32.33. The protein encoded by this gene is a member of the BAG1-related protein family. BAG1 is believed to be an anti-apoptotic protein that may function through interactions with a variety of cell apoptosis and growth related proteins including BCL-2, Raf-protein kinase, steroid hormone receptors, growth factor receptors and members of the heat shock protein 70 kDa family. The protein encoded by BAG5 gene contains a BAG domain near the C-terminus, which may bind and inhibit the chaperone activity of Hsc70/Hsp70.

[0473] Nucleotides 3913 to 4117 of SEQ ID NO: 321 show 82% sequence identity with an intron sequence of DNAH11. DNAH11 encodes dynein, axonemal, heavy polypeptide 11. The gene has LocusID: 8701, and is reportedly located on chromosome 7p21.

[0474] CPS 290 corresponds to UNK_AL022721 (RPL10A) which encodes ribosomal protein L10a. RPL10A has LocusID: 4736, and is located on chromosome 6 with reported cytogenetic location 6p21.3-p21.2. The gene product is a component of the large 60S ribosomal subunit.

[0475] CPS 290 also has 96% sequence identity with LOC253986 and LOC137107, both of which encode proteins similar to ribosomal protein L10a. LOC253986 is located on chromosome 8, and LOC137107 is located at chromosome 8p11.23. In addition, CPS 290 has about 90-96% sequence identity with intron sequences of PTPRG, BST1, and MARK3. PTPRG encodes protein tyrosine phosphatase, receptor type, G. PTPRG has LocusID: 5793, and is located at chromosome 3p21-p14. BST1 encodes bone marrow stromal cell antigen 1, and has LocusID: 683 with reported cytogenetic location 4p15. MARK3 encodes MAP/microtubule affinity-regulating kinase 3, and has LocusID: 4140 with reported cytogenetic location 14q32.3. CPS 290 aligns to LOC138030 with 84% sequence identity. LOC138030 encodes a protein similar to ribosomal protein L10a, and is located at chromosome 8p21.3.

[0476] CPS 290 (SEQ ID NO: 329) is a spliced product of the complement of nucleotides 26623 to 27200 of SEQ ID NO: 322. Blast search against the Entrez human genome database shows that SEQ ID NO: 322 has 100% sequence identity with a chromosomal region on chromosome 6. This chromosomal region is located within Genomic Locus NT_007592, and includes the following genes: TEAD3, RPL10A, FANCE, LOC221485, and LOC221486. TEAD3 encodes TEA domain family member 3, and has LocusID: 7005. RPL10A encodes ribosomal protein L10a, and has LocusID: 4736. FANCE encodes Fanconi anemia, complementation group E, and has LocusID: 2178. LOC221485 encodes a protein similar to dJ109F14.3 (PUTATIVE ZNF127 LIKE protein). LOC221486 encodes a protein similar to Peroxisome proliferator activated receptor beta (PPAR-beta) (PPAR-delta) (Nuclear hormone receptor 1) (NUC1) (NUC1). SEQ ID NO: 322 aligns to the protein-coding strand of TEAD3, while aligning to the non-protein-coding strands of RPL10A, FANCE, LOC221485, and LOC221486.

[0477] Fragments of SEQ ID NO: 322 show various degrees of sequence identity with a plurality of chromosomal regions through the human genome.

[0478] CPS 291 corresponds to DKZP586E0820 (PKD2) which encodes protein kinase D2. The gene has LocusID: 25865, and is located on chromosome 19 with reported cytogenetic location 19q13.2. The gene product is similar to a region of mu isoforms of protein kinase C, and may function to mediate protein-protein and protein-lipid interaction. The gene product contains a kinase domain and a pleckstrin homology (PH) domain.

[0479] CPS 292 corresponds to NONO which encodes non-POU domain containing, octamer-binding. The gene has LocusID: 4841, and is located on chromosome X with

reported cytogenetic location Xq13.1. The gene product is a nuclear protein which contains RNA recognition motifs.

[0480] SEQ ID NO: 324 also aligns to LOC146455 with about 95-96% sequence identity. LOC146455 encodes a protein similar to 54 kDa nuclear RNA- and DNA-binding protein (p54(nrb)) (p54nrb) (55 kDa nuclear protein) (NMT55) (Non-POU domain-containing octamer-binding protein) (DNA-binding P52/P100 complex, 52 kDa subunit). LOC146455 is located at chromosome 16q22.3. In addition, nucleotides 514 to 2591 of SEQ ID NO: 324 have about 84-85% sequence identity with a chromosomal region which overlaps LOC130867. LOC130867 encodes a protein similar to ribosomal protein S12 (40S ribosomal protein S12), and is located at chromosome 2p15.

[0481] CPS 293 corresponds to UNK_AI743507 (ZFR) which encodes zinc finger RNA binding protein. ZFR has LocusID: 51663, and is located on chromosome 5 with reported cytogenetic location 5p13.2.

[0482] CPS 293 also shows 92% sequence identity with LOC119355 which encodes a protein similar to M-phase phosphoprotein homolog; likely ortholog of mouse zinc finger protein Zfr. LOC119355 has reported cytogenetic location 10q23.33. In addition, CPS 293 has 94-96% sequence identity with a chromosomal region on chromosome 1. The chromosomal region is close to TSNA-X which encodes translin-associated factor X and has LocusID: 7257 and cytogenetic location 1q42.1. Nucleotides 292 to 399 of CPS 293 have about 92% sequence identity with a chromosomal region on chromosome 1.

[0483] CPS 294 corresponds to MAPKAPK5 which encodes mitogen-activated protein kinase-activated protein kinase 5. The gene has LocusID: 8550, and is located on chromosome 12 with reported cytogenetic location 12q24.12. The protein encoded by this gene is a member of the serine/threonine kinase family. In response to cellular stress and proinflammatory cytokines, this kinase may be activated through its phosphorylation by MAP kinases including MAPK1/ERK, MAPK14/p38-alpha, and MAPK11/p38-beta. At least two alternately spliced transcript variants of this gene encoding distinct isoforms have been reported.

[0484] CPS 295 corresponds to UNK_U79297 (LOC157567) which encodes a protein similar to hypothetical protein MGC25673. LOC157567 is reportedly located at chromosome 8q23.1.

[0485] The significance of the RCC disease genes listed in Table 4 can be estimated using a relative class separation metric according to the supervised classification of RCC

versus disease-free. See Golub, *et al.*, Science, 286: 531-537 (1999), and Slonim, *et al.*, Procs. of the Fourth Annual International Conference on Computational Molecular Biology, Tokyo, Japan, April 8 - 11, p263-272 (2000). A neighborhood analysis can then be performed to determine the significance of the measured correlations. For instance, this method can randomly permute the 65 total sample (45 RCC patients and 20 disease-free humans) into two groups of 45 and 20 samples each and then rank the genes with the highest measures of correlation in the 100 randomized sets of samples. This analysis shows that a majority of RCC disease genes identified in the present invention possess measures or correlation above the 1% significant level compared to randomly permuted class vectors.

[0486] The biological mechanisms underlying the differential expression patterns of the RCC disease genes in the peripheral blood are not fully understood. The differential expression patterns may be attributed to the altered gene expression patterns in shed RCC tumor cells in the peripheral blood. For instance, Table 5 shows that a subset of the RCC disease genes are also differentially expressed in RCC tumor cells compared to PBMCs of disease-free humans. The differential expression pattern may also be caused by immunogenic reactions induced by RCC tumors. In one experiment, peripheral blood mononuclear cells are isolated from disease-free humans and then treated with phytohemagglutinin (PHA). PHA stimulation *ex vivo* appears to recapitulate the differential expression pattern of a significant number of the RCC disease genes of this invention, as illustrated in Table 5. This suggests that the differential expression patterns of some RCC disease genes in the peripheral blood may arise from an activation of leukocytes *in vivo*.

[0487] Table 5 further identifies a substantial subset of RCC disease genes that are differentially expressed in patients with end-stage renal failure. Therefore, the differential expression patterns of this subset of RCC disease genes in the peripheral blood could be due to alterations in leukocytes in response to renal dysfunction in RCC patients.

Table 5. RCC Disease Genes Differentially Expressed Under Other Conditions

RCC Disease Gene	Entrez Accession No.	Differentially Expressed in: (compared to disease-free PBMCs)
IL1R1	M27492	Ex vivo PHA-stimulated PBMCs
CSF2	M13207	Ex vivo PHA-stimulated PBMCs
IL1B		Ex vivo PHA-stimulated PBMCs
Tubulin, Beta	AF141349	Ex vivo PHA-stimulated PBMCs

RCC Disease Gene	Entrez Accession No.	Differentially Expressed in: (compared to disease-free PBMCs)
BASP1	AA135683	Ex vivo PHA-stimulated PBMCs
SIAH2	U76248	Ex vivo PHA-stimulated PBMCs
GSPT1	X17644	Ex vivo PHA-stimulated PBMCs
SCYA2	M28225	Ex vivo PHA-stimulated PBMCs
BCL2L1	Z23115	Ex vivo PHA-stimulated PBMCs
BAG1	Z35491	Ex vivo PHA-stimulated PBMCs
PAI2	Y00630	Ex vivo PHA-stimulated PBMCs
HPGD	X82460	Ex vivo PHA-stimulated PBMCs
CTSL	X12451	Ex vivo PHA-stimulated PBMCs
IL6	X04430	Ex vivo PHA-stimulated PBMCs
TUBB	X79535	Ex vivo PHA-stimulated PBMCs
SCYA7	X72308	Ex vivo PHA-stimulated PBMCs
DRD2	X51362	Ex vivo PHA-stimulated PBMCs
SCYA2	M26683	Ex vivo PHA-stimulated PBMCs
FABP5	M94856	Ex vivo PHA-stimulated PBMCs / RCC Tumor Tissue
SCYA20	U64197	Ex vivo PHA-stimulated PBMCs / RCC Tumor Tissue
ADM	D14874	Ex vivo PHA-stimulated PBMCs / RCC Tumor Tissue / Renal Failure PBMCs
COPEB	AF001461	Ex vivo PHA-stimulated PBMCs / RCC Tumor Tissue / Renal Failure PBMCs
AQP9	AB008775	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
PTGS2	U04636	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
STIP1	M86752	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
SOD2	X07834	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
PDXK	U89606	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
IL1RN	X52015	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
ANXA5	U05770	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs

RCC Disease Gene	Entrez Accession No.	Differentially Expressed in: (compared to disease-free PBMCs)
IFIT4	AF026939	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
IL1B	M15330	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
GRO1	X54489	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
PLAUR	X74039	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
NP	X00737	Ex vivo PHA-stimulated PBMCs / Renal Failure PBMCs
FCGR3B	X16863	RCC Tumor Tissue
UNK_M62896	M62896	RCC Tumor Tissue
FN1	X02761	RCC Tumor Tissue
HMOX1	Z82244	RCC Tumor Tissue
ITGA7	AF032108	RCC Tumor Tissue
DGCR5	X91348	RCC Tumor Tissue
CBP2	D83174	RCC Tumor Tissue
UNK_AL049250	AL049250	RCC Tumor Tissue
SLC1A4	AA978353	RCC Tumor Tissue
MMP9	J05070	RCC Tumor Tissue / Renal Failure PBMCs
SLC16A3	U81800	RCC Tumor Tissue / Renal Failure PBMCs
LILRB3	AF025533	RCC Tumor Tissue / Renal Failure PBMCs
FCGR1A	M63835	RCC Tumor Tissue / Renal Failure PBMCs
LHFPL2	D86961	RCC Tumor Tissue / Renal Failure PBMCs
PLEC1	U53204	RCC Tumor Tissue / Renal Failure PBMCs
S100A11	D38583	RCC Tumor Tissue / Renal Failure PBMCs
SPOP	AJ000644	RCC Tumor Tissue / Renal Failure PBMCs
CCR1	D10925	RCC Tumor Tissue / Renal Failure PBMCs
TLR2	AF051152	RCC Tumor Tissue / Renal Failure PBMCs
KIAA0750	AB018293	RCC Tumor Tissue / Renal Failure PBMCs

RCC Disease Gene	Entrez Accession No.	Differentially Expressed in: (compared to disease-free PBMCs)
CDC34	L22005	Renal Failure PBMCs
POLR2J	L37127	Renal Failure PBMCs
ETS2	J04102	Renal Failure PBMCs
MAD	L06895	Renal Failure PBMCs
GPR3	L32831	Renal Failure PBMCs
PIP5K1C	AB011161	Renal Failure PBMCs
PRF1	M28393	Renal Failure PBMCs
PSMA7	AF054185	Renal Failure PBMCs
INPP4A	U96919	Renal Failure PBMCs
TCFL1	D43642	Renal Failure PBMCs
DGAT	AF059202	Renal Failure PBMCs
S100P	AA131149	Renal Failure PBMCs
DOC-1R	AF089814	Renal Failure PBMCs
C8FW	AJ000480	Renal Failure PBMCs
PDI2	AB023211	Renal Failure PBMCs
GEF-2	AI565760	Renal Failure PBMCs
TNNT1	M19309	Renal Failure PBMCs
BSG	X64364	Renal Failure PBMCs
IL17R	U58917	Renal Failure PBMCs
HK3	U51333	Renal Failure PBMCs
RALBP1	L42542	Renal Failure PBMCs
RNASE2	X55988	Renal Failure PBMCs
TPM1	M19267	Renal Failure PBMCs
BLVRB	D32143	Renal Failure PBMCs
APS	AB000520	Renal Failure PBMCs
PPARD	L07592	Renal Failure PBMCs
NFE2	S77763	Renal Failure PBMCs
IL1RAP	AB006537	Renal Failure PBMCs
ETS2	AF017257	Renal Failure PBMCs

RCC Disease Gene	Entrez Accession No.	Differentially Expressed in: (compared to disease-free PBMCs)
S100A12	D83664	Renal Failure PBMCs
CD9	M38690	Renal Failure PBMCs
ENIGMA	L35240	Renal Failure PBMCs
HAGH	X90999	Renal Failure PBMCs
NCF1	M55067	Renal Failure PBMCs
FLOT1	AF089750	Renal Failure PBMCs
ITGA2B	M34480	Renal Failure PBMCs
FKBP8	L37033	Renal Failure PBMCs
DUSP6	AB013382	Renal Failure PBMCs
CBFA2T3	AB010419	Renal Failure PBMCs

C. Other Solid Tumor Disease Genes

[0488] The methodologies described in subsection B can be easily adapted to the identification of other solid tumor disease genes. These solid tumor disease genes are differentially expressed in the peripheral blood or PBMCs of solid tumor patients compared to disease-free humans.

[0489] In one embodiment, the genechip expression data derived from PBMC-enriched peripheral blood samples of RCC, prostate cancer, head/neck cancer and disease-free humans is collected, compared and analyzed using a multi-class correlation metric. The multi-class correlation metric can identify and rank the genes mostly highly correlated with each class of the peripheral blood gene expression profiles. Suitable multi-class correlation metrics include, but are not limited to, the GeneCluster 2 software provided by MIT Center for Genome Research at Whitehead Institute (Cambridge, MA). The GeneCluster 2 software has supervised classification, gene selection and permutation test functions. It includes algorithms for building and testing supervised models using weighted voting and k-nearest neighbors algorithms.

[0490] In one example, a 20-gene set is selected using 70% of the expression profiles as a training set. These 20 multi-class classifier genes are listed in Table 10. Each of these 20 genes has a differential expression pattern in the peripheral blood of all three classes of solid tumor patients (*i.e.*, RCC, prostate cancer and head/neck cancer) as

compared to disease-free humans. The gene set has over 89% prediction accuracy for each remaining profile. Other gene sets with high predication accuracy for RCC, prostate cancer, head/neck cancer and disease-free can be similarly obtained.

[0491] In another embodiment, a multi-class correlation metric is used to identify genes capable of predicting solid tumor versus solid tumor-free, regardless of the particular type of the solid tumor. The peripheral blood gene expression profiles from RCC, prostate cancer, head/neck cancer, and disease-free humans are analyzed using multi-class comparison. A 19-gene set is selected using 70% of the total samples as a training set. The gene set thus selected is listed in Table 11. Each gene in the gene set is differentially expressed in the peripheral blood of all three types of solid tumor patients (RCC, prostate cancer, and head/neck cancer) as compared to disease-free humans. This 19-gene set is capable of accurately predicting solid tumor versus solid tumor-free for the remaining expression profiles. Other gene sets with high prediction accuracy for solid tumor versus solid tumor-free can be similarly obtained.

D. Detecting RCC, RCC-Free, Solid Tumor and/or Solid Tumor-Free

[0492] The RCC disease genes identified in Table 4 can be used to detect RCC, RCC-free, solid tumors, and/or solid tumor-free in a human subject with unknown disease status. For instance, if the expression patterns of one or more RCC disease genes in the peripheral blood sample of the human subject are not substantially different from the corresponding expression patterns in disease-free humans, then it is suggestive that the human subject under diagnosis is RCC-free. Conversely, if the expression patterns of one or more RCC disease genes in the human subject are substantially different from the corresponding expression patterns in disease-free humans (e.g., gene expression levels in the human subject are substantially higher or lower than those in disease-free humans), then it is suggestive that the human subject may be infected with RCC (or other solid tumors, depending on the genes used in the diagnosis). Algorithms, such as the weighted voting programs, can be used to facilitate the diagnosis. In addition, other clinical evidence can be combined with the gene-based test to reduce the risk of false diagnosis. Similar approaches can be used to predict the presence or absence of other solid tumors such as prostate cancer and head/neck cancer.

[0493] Diagnostic or screening methods based on differentially expressed gene products are well known in the art. In accordance with one aspect of the present invention, the differential expression patterns of RCC disease genes can be determined by measuring the levels of RNA transcripts of these genes in peripheral blood samples. Suitable methods for this purpose include, but are not limited to, RT-PCT, Northern Blot, *in situ* hybridization, Southern Blot, slot-blotting, nuclease protection assay and polynucleotide arrays. The peripheral blood samples can be either whole blood, or blood samples containing enriched PBMCs.

[0494] In general, RNA isolated from peripheral blood samples can be amplified to cDNA or cRNA before detection and/or quantitation. The isolated RNA can be either total RNA or mRNA. The RNA amplification can be specific or non-specific. Suitable amplification methods include, but are not limited to, reverse transcriptase PCR, isothermal amplification, ligase chain reaction, and Qbeta replicase. The amplified nucleic acid products can be detected and/or quantitated through hybridization to labeled probes.

[0495] Amplification primers or hybridization probes for an RCC disease gene can be prepared from the gene sequence or its corresponding CPS using methods well known in the art. Gene sequences suitable for this purpose include, but are not limited to, exons, introns, or the 3' or 5' untranslated regions, or any combination thereof. In one embodiment, the probes or primers are designed based on the sequence in or near the 3' protein-coding region of the RCC disease gene. For instance, the nucleotide sequence encoding the last 100 to 300 amino acid residues in the C-terminus region of the RCC disease gene product can be selected to design probes or primers. In the case that the genomic location(s) of the RCC disease gene has not been determined or that the gene may correspond to multiple genomic loci, the probes/primers can be designed based on the CPS of the gene, or the oligonucleotide probes on the HG-U95Av2 gene chip that was used for the identification of the gene.

[0496] Table 4 lists sequences suitable for making probes/primers for the detection of their corresponding RCC disease genes. Examples of suitable oligonucleotide probes/primers are listed in ATTACHMENT A.

[0497] In one embodiment, each probe/primer comprises at least 15 nucleotides. For instance, each probe can comprise at least 20, 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 400 or more nucleotides. Preferably, each probe/primer has relatively high sequence complexity and does not have any ambiguous residue

(undetermined "n" residues). The probes/primers preferably can hybridize to the target gene, including its RNA transcripts, under stringent or highly stringent conditions.

[0498] In another embodiment, the probes/primers for a gene are selected from regions which significantly diverge from the sequences of other genes. Such regions can be determined by checking the probe/primer sequences against a human genome sequence database, such as the Entrez database at the NCBI. One algorithm suitable for this purpose is the BLAST algorithm. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence to increase the cumulative alignment score. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. These parameters can be adjusted for different purposes, as appreciated by one of ordinary skill in the art.

[0499] In a preferred embodiment, quantitative RT-PCR (such as TaqMan, ABI) is used for detecting and comparing the levels of RNA transcripts of the RCC disease genes in peripheral blood samples. Quantitative RT-PCR involves reverse transcription (RT) of RNA to cDNA followed by relative quantitative PCR (RT-PCR).

[0500] In PCR, the number of molecules of the amplified target DNA increases by a factor approaching two with every cycle of the reaction until some reagent becomes limiting. Thereafter, the rate of amplification becomes increasingly diminished until there is not an increase in the amplified target between cycles. If one plots a graph on which the cycle number is on the X axis and the log of the concentration of the amplified target DNA is on the Y axis, one observes that a curved line of characteristic shape is formed by connecting the plotted points. Beginning with the first cycle, the slope of the line is positive and constant. This is said to be the linear portion of the curve. After some reagent becomes limiting, the slope of the line begins to decrease and eventually becomes zero. At this point the concentration of the amplified target DNA becomes asymptotic to some fixed value. This is said to be the plateau portion of the curve.

[0501] The concentration of the target DNA in the linear portion of the PCR is proportional to the starting concentration of the target before the PCR was begun. By determining the concentration of the PCR products of the target DNA in PCR reactions that have completed the same number of cycles and are in their linear ranges, it is possible to determine the relative concentrations of the specific target sequence in the original DNA mixture. If the DNA mixtures are cDNAs synthesized from RNAs isolated from different tissues or cells, the relative abundances of the specific mRNA from which the target sequence was derived may be determined for the respective tissues or cells. This direct proportionality between the concentration of the PCR products and the relative mRNA abundances is true in the linear range portion of the PCR reaction.

[0502] The final concentration of the target DNA in the plateau portion of the curve is determined by the availability of reagents in the reaction mix and is independent of the original concentration of target DNA. Therefore, the sampling and quantifying of the amplified PCR products preferably are carried out when the PCR reactions are in the linear portion of their curves. In addition, relative concentrations of the amplifiable cDNAs preferably are normalized to some independent standard, which may be based on either internally existing RNA species or externally introduced RNA species. The abundance of a particular mRNA species may also be determined relative to the average abundance of all mRNA species in the sample.

[0503] In one embodiment, the PCR amplification utilizes internal PCR standards that are approximately as abundant as the target. This strategy is effective if the products of the PCR amplifications are sampled during their linear phases. If the products are sampled when the reactions are approaching the plateau phase, then the less abundant product may become relatively over-represented. Comparisons of relative abundances made for many different RNA samples, such as is the case when examining RNA samples for differential expression, may become distorted in such a way as to make differences in relative abundances of RNAs appear less than they actually are. This can be improved if the internal standard is much more abundant than the target. If the internal standard is more abundant than the target, then direct linear comparisons may be made between RNA samples.

[0504] A problem inherent in clinical samples is that they are of variable quantity and/or quality. This problem can be overcome if the RT-PCR is performed as a relative quantitative RT-PCR with an internal standard in which the internal standard is an

amplifiable cDNA fragment that is larger than the target cDNA fragment and in which the abundance of the mRNA encoding the internal standard is roughly 5-100 fold higher than the mRNA encoding the target. This assay measures relative abundance, not absolute abundance of the respective mRNA species.

[0505] In another embodiment, the relative quantitative RT-PCR uses an external standard protocol. Under this protocol, the PCR products are sampled in the linear portion of their amplification curves. The number of PCR cycles that are optimal for sampling can be empirically determined for each target cDNA fragment. In addition, the reverse transcriptase products of each RNA population isolated from the various samples can be normalized for equal concentrations of amplifiable cDNAs. While empirical determination of the linear range of the amplification curve and normalization of cDNA preparations are tedious and time-consuming processes, the resulting RT-PCR assays may, in certain cases, be superior to those derived from a relative quantitative RT-PCR with an internal standard.

[0506] Nucleic acid arrays can also be used to detect and compare the differential expression patterns of RCC disease genes in peripheral blood samples. The probes suitable for detecting the corresponding RCC disease genes can be stably attached to known discrete regions on a solid substrate. As used herein, a probe is "stably attached" to a discrete region if the probe maintains its position relative to the discrete region during the hybridization and the subsequent washes. Construction of nucleic acid arrays is well known in the art. Suitable substrates for making polynucleotide arrays include, but are not limited to, membranes, films, plastics and quartz wafers.

[0507] A nucleic acid array of the present invention can comprise at least 2, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more different polynucleotide probes, each different probe capable of hybridizing to a different respective RCC disease gene. Multiple probes for the same gene can be used on a single nucleic acid array. Examples of probes suitable for this invention are listed in ATTACHMENT A. Probes for other disease genes can also be included in the nucleic acid array of this invention. The probe density on the array can be in any range. For instance, the density may be 50, 100, 200, 300, 400, 500 or more probes/cm².

[0508] In one embodiment, nuclease protection assays are used to quantify RNAs derived from the peripheral blood samples. There are many different versions of nuclease protection assays known to those practiced in the art. The common characteristic that these nuclease protection assays is that they involve hybridization of an antisense nucleic acid

with the RNA to be quantified. The resulting hybrid double-stranded molecule is then digested with a nuclease that digests single-stranded nucleic acids more efficiently than double-stranded molecules. The amount of antisense nucleic acid that survives digestion is a measure of the amount of the target RNA species to be quantified. An example of a nuclease protection assay that is commercially available is the RNase protection assay manufactured by Ambion, Inc. (Austin, Texas).

[0509] The above-described methods can also be used to determine the levels of RNA species in the peripheral blood that are capable of hybridizing to the CPSs listed in CPS-Table-2. The levels of these RNA species in the peripheral blood can be indicative as to whether a human subject has RCC or is RCC-free.

[0510] In accordance with another aspect of the present invention, the differential expression patterns of RCC disease genes can be determined by measuring the levels of polypeptides encoded by these genes in peripheral blood. Methods suitable for this purpose include, but are not limited to, immunoassays such as ELISA, RIA, FACS, dot blot, Western Blot, immunohistochemistry, and antibody-based radioimaging. Protocols for carrying out these immunoassays are well known in the art. Other methods such as 2-dimensional SDS-polyacrylamide gel electrophoresis can also be used.

[0511] One exemplary method suitable for detecting the levels of target proteins in peripheral blood samples is ELISA. In an exemplifying ELISA, antibodies capable of binding to the target proteins encoded by one or more RCC disease genes are immobilized onto a selected surface exhibiting protein affinity, such as wells in a polystyrene or polyvinylchloride microtiter plate. Then, peripheral blood samples to be tested are added to the wells. After binding and washing to remove non-specifically bound immunocomplexes, the bound antigen(s) can be detected. Detection can be achieved by the addition of a second antibody which is specific for the target proteins and is linked to a detectable label. Detection may also be achieved by the addition of a second antibody, followed by the addition of a third antibody that has binding affinity for the second antibody, with the third antibody being linked to a detectable label. Before being added to the microtiter plate, cells in the peripheral blood samples can be lysed using various methods known in the art. Proper extraction procedures can be used to separate the target proteins from potentially interfering substances.

[0512] In another exemplifying ELISA, the peripheral blood samples suspected of containing the target proteins are immobilized onto the well surface and then contacted with

the antibodies of the invention. After binding and washing to remove non-specifically bound immunocomplexes, the bound antigen is detected. Where the initial antibodies are linked to a detectable label, the immunocomplexes can be detected directly. The immunocomplexes can also be detected using a second antibody that has binding affinity for the first antibody, with the second antibody being linked to a detectable label.

[0513] Another exemplary ELISA involves the use of antibody competition in the detection. In this ELISA, the target proteins are immobilized on the well surface. The labeled antibodies are added to the well, allowed to bind to the target proteins, and detected by means of their labels. The amount of the target proteins in an unknown sample is then determined by mixing the sample with the labeled antibodies before or during incubation with coated wells. The presence of the target proteins in the unknown sample acts to reduce the amount of antibody available for binding to the well and thus reduces the ultimate signal.

[0514] Different ELISA formats can have certain features in common, such as coating, incubating or binding, washing to remove non-specifically bound species, and detecting the bound immunocomplexes. For instance, in coating a plate with either antigen or antibody, the wells of the plate can be incubated with a solution of the antigen or antibody, either overnight or for a specified period of hours. The wells of the plate are then washed to remove incompletely adsorbed material. Any remaining available surfaces of the wells are then "coated" with a nonspecific protein that is antigenically neutral with regard to the test samples. Examples of these nonspecific proteins include bovine serum albumin (BSA), casein and solutions of milk powder. The coating allows for blocking of nonspecific adsorption sites on the immobilizing surface and thus reduces the background caused by nonspecific binding of antisera onto the surface.

[0515] In ELISAs, a secondary or tertiary detection means can also be used. After binding of a protein or antibody to the well, coating with a non-reactive material to reduce background, and washing to remove unbound material, the immobilizing surface is contacted with the control and/or clinical or biological sample to be tested under conditions effective to allow immunocomplex (antigen/antibody) formation. These conditions may include, for example, diluting the antigens and antibodies with solutions such as BSA, bovine gamma globulin (BGG) and phosphate buffered saline (PBS)/Tween and incubating the antibodies and antigens at room temperature for about 1 to 4 hours or at 4°C overnight. Detection of the immunocomplex then requires a labeled secondary binding ligand or

antibody, or a secondary binding ligand or antibody in conjunction with a labeled tertiary antibody or third binding ligand.

[0516] Following all incubation steps in an ELISA, the contacted surface can be washed so as to remove non-complexed material. For instance, the surface may be washed with a solution such as PBS/Tween, or borate buffer. Following the formation of specific immunocomplexes between the test sample and the originally bound material, and subsequent washing, the occurrence of the amount of immunocomplexes can be determined.

[0517] To provide a detecting means, the second or third antibody can have an associated label to allow detection. In one embodiment, the label is an enzyme that generates color development upon incubating with an appropriate chromogenic substrate. Thus, for example, one may contact and incubate the first or second immunocomplex with a urease, glucose oxidase, alkaline phosphatase or hydrogen peroxidase-conjugated antibody for a period of time and under conditions that favor the development of further immunocomplex formation (e.g., incubation for 2 hours at room temperature in a PBS-containing solution such as PBS-Tween).

[0518] After incubation with the labeled antibody, and subsequent to washing to remove unbound material, the amount of label is quantified, e.g., by incubation with a chromogenic substrate such as urea and bromocresol purple or 2,2'-azido-di-(3-ethyl)-benzthiazoline-6-sulfonic acid (ABTS) and H_2O_2 , in the case of peroxidase as the enzyme label. Quantitation can be achieved by measuring the degree of color generation, e.g., using a spectrophotometer.

[0519] Another method suitable this invention is RIA (radioimmunoassay). An exemplary RIA is based on the competition between radiolabeled-polypeptides and unlabeled polypeptides for binding to a limited quantity of antibodies. Suitable radiolabels include, but are not limited to, I^{125} . In one embodiment, a fixed concentration of I^{125} -labeled polypeptide is incubated with a series of dilution of an antibody specific to the polypeptide. When the unlabeled polypeptide is added to the system, the amount of the I^{125} -polypeptide that binds to the antibody is decreased. A standard curve can therefore be constructed to represent the amount of antibody-bound I^{125} -polypeptide as a function of the concentration of the unlabeled polypeptide. From this standard curve, the concentration of the polypeptide in unknown samples can be determined. Various protocols for conducting RIA to measure the levels of polypeptides in peripheral blood samples are well known in the art.

[0520] Suitable antibodies for this invention include, but are not limited to, polyclonal antibodies, monoclonal antibodies, chimeric antibodies, humanized antibodies, single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (*i.e.*, those which inhibit dimer formation) can also be used.

[0521] Polyclonal antibodies can be prepared by immunizing a suitable subject with RCC disease gene products or fragments thereof. The antibody titer in the immunized subject can be monitored over the time using standard techniques, such as ELISA. The antibodies can be isolated from the immunized subject using techniques well known in the art.

[0522] In one embodiment, hybridomas capable of producing antibodies against RCC disease gene products are prepared. RCC disease gene products can be prepared using bacteria or other cells transformed or transfected with the polynucleotide sequences encoding the gene products. The purified gene products, or fragments thereof, are used to immunize a vertebrate, such as a mammal. Suitable mammals include mice, rabbits and sheep. Preferably, the fragment used for immunization comprises at least 8 amino acid residues, more preferably at least 12 amino acid residues, highly preferably at least 16 amino acid residues, and most preferably at least 20 amino acid residues.

[0523] Immunogenic fragments (epitopes) in the gene products can be identified using known techniques. Preferred epitopes are regions that are located on the surfaces of the gene products. These regions are usually hydrophilic.

[0524] Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line (such as a myeloma) to form hybridomas. Preferably, the immortal cell line is derived from the same mammalian species as the lymphocytes. For example, murine hybridomas can be made by fusing an immortalized mouse cell line with lymphocytes isolated from a mouse that is immunized with an immunogenic preparation of the present invention. Preferred immortalized cell lines include mouse myeloma cell lines that are sensitive to culture medium containing hypoxanthine, aminopterin and thymidine ("HAT medium"). Suitable myeloma cell lines include, but are not limited to, the P3-NS1/l-Ag4-1, P3-x63-Ag8.653 or Sp210-Ag14 myeloma lines, all of which are available from ATCC. In one embodiment, HAT-sensitive mouse myeloma cells are fused to mouse splenocytes using polyethylene glycol ("PEG"). Hybridoma cells thus produced are selected against HAT medium, which kills unfused or unproductively fused myeloma cells.

Hybridoma cells which produce monoclonal antibodies against the RCC disease gene products can be detected by screening the hybridoma culture supernatants.

[0525] Monoclonal antibodies can also be prepared by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phase display library). Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP™ Phage Display Kit*, Catalog No. 240612).

[0526] The antibodies suitable for this invention also include "single-chain Fv" or "scFv." The scFv fragments comprise the V_H and V_L domains of an antibody. Generally, the scFv polypeptide further comprises a polypeptide linker between the V_H and V_L domains. The polypeptide linker enables the scFv to form the desired structure for antigen binding. Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, can be prepared, as appreciated by one of ordinary skill in the art.

[0527] Humanized antibodies can also be used. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains, or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies are derived from human immunoglobulins in which the residues forming the complementary determining regions (CDRs) are replaced by the residues from CDRs of a non-human antibody, such as a mouse, rat or rabbit antibody having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. The humanized antibody can comprise at least one or two variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the constant regions are those of a human immunoglobulin consensus sequence. The humanized antibody preferably comprises at least a portion of an immunoglobulin constant region (Fc) of a human immunoglobulin.

[0528] Humanized antibodies can be produced using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains but can express human heavy and light chains. The transgenic mice are immunized in the normal fashion with a selected antigen. Monoclonal antibodies directed against the antigen can be obtained

using conventional hybridoma technology. The human immunoglobulin transgenes harbored in the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Using this technique, therapeutically useful IgG, IgA and IgE antibodies can be prepared.

[0529] In addition, humanized antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, *e.g.*, a murine antibody, is used to guide the selection of a humanized antibody recognizing the same epitope.

[0530] In one embodiment, the antibodies of the present invention can bind to the corresponding RCC disease gene products or the desired antigens with a binding affinity constant K_a of at least $10^4 M^{-1}$, such as at least $10^5 M^{-1}$, $10^6 M^{-1}$, $10^7 M^{-1}$ or more.

[0531] The antibodies of this invention can be labeled with one or more detectable moieties to allow for detection of antibody-antigen complexes. The detectable moieties can include compositions detectable by spectroscopic, enzymatic, photochemical, biochemical, bioelectronic, immunochemical, electrical, optical or chemical means. The detectable moieties include, but are not limited to, radioisotopes, chemiluminescent compounds, labeled binding proteins, heavy metal atoms, spectroscopic markers such as fluorescent markers and dyes, magnetic labels, linked enzymes, mass spectrometry tags, spin labels, electron transfer donors and acceptors, and the like.

[0532] In accordance with yet another aspect of the present invention, the levels of polypeptides in peripheral blood samples can be determined by detecting the biological activities associated with the polypeptides. If a biological function/activity of a polypeptide is known, suitable *in vitro* bioassays can be designed to evaluate the biological function/activity, thereby determining the amount of the polypeptide in the sample.

[0533] The expression levels of RCC disease genes or the respective CPSs can be compared to the reference expression levels using various methods. These reference levels can be determined using peripheral blood samples isolated from disease-free humans, RCC or other solid tumor patients. The comparison can be performed using the fold change or the absolute difference between the expression levels to be compared. One or more RCC disease genes or CPSs can be used in the comparison. For instance, at least 2, 3, 4, 6, 8, 10, 12, 14, 16, 18, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more RCC disease genes or CPSs can be used.

[0534] The expression patterns can also be compared by using one or more ratios between the expression levels of different disease genes. Other suitable measures or indicators can also be employed for assessing the relationship or difference between different expression patterns.

[0535] The use of multiple CPSs or RCC disease genes can reduce the risk of false prediction. In one embodiment, if more than 50% (such as 60%, 70%, 80% or 90%) of the selected CPSs or RCC disease genes suggest that the test human has RCC or is RCC-free, then a prediction for RCC or RCC-free will be made respectively. In another embodiment, the gene expression-based comparison is combined with other clinical evidence in predicting RCC and/or other solid tumors.

[0536] In a preferred embodiment, the RCC disease genes used for predicting RCC versus RCC-free include or consist of one or more genes selected from the group consisting of EEF1A2, TLR2, BRF2, LGALS3, SNRPG, DKFZP586E1621, NUMA1, SOD2, AKR1B1, DUSP6, SMARCE1, KIAA0669, MSF, IL1RN, PTMA, KIAA0410, PSMD3, T54, C1QBP, and OSR1. For instance, the RCC disease genes used for RCC prediction can include or consist of at least 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 genes selected from the group. For another instance, the RCC disease genes used for diagnosis can comprise (1) at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 genes selected from the group consisting of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, KIAA0410, T54 and OSR1, and/or (2) at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 genes selected from the group consisting of EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, MSF, PTMA, PSMD3 and C1QBP.

[0537] In another preferred embodiment, the CPSs used for predicting RCC versus RCC-free include or consist of one or more CPSs selected from the group consisting of CPS 1, CPS 3, CPS 4, CPS 6, CPS 18, CPS 38, CPS 53, CPS 255, CPS256, CPS 257, CPS 258, CPS 259, CPS 260, CPS 261, CPS 262, CPS 263, CPS 264, CPS 265, CPS 266, and CPS 267. For instance, the CPSs used for RCC prediction can include or consist of at least 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 CPSs selected from the group. For another instance, the CPSs used for diagnosis can comprise (1) at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 CPSs selected from the group consisting of CPS 1, CPS 3, CPS 4, CPS 6, CPS 18, CPS 38, CPS 53, CPS 261, CPS 264 and CPS 267, and/or (2) at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 CPSs selected from the group consisting of CPS 255, CPS 256, CPS 257, CPS 258, CPS 259, CPS 260, CPS 262, CPS 263, CPS 265, and CPS 266.

[0538] In yet another preferred embodiment, the RCC disease genes used for predicting RCC versus RCC-free include or consist of one or more genes selected from the group consisting of CD44, KIAA0410, MARCO, MAP3K8, NSP-CL, PIP5K1C, NRG1, RAB31, LGALS3, MEF2D, ITGA7, LHFPL2, ETS2, KHSRP, ENIGMA, UNK_AF038187, RAB13, TLR2, T54 and DUSP6. For instance, the RCC disease genes used for prediction can include or consist of at least 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 genes selected from the group.

[0539] In still another preferred embodiment, the CPSs used for predicting RCC versus RCC-free include or consist of one or more CPSs selected from the group consisting of CPSs 1, 3, 4, 5, 6, 7, 9, 10, 11, 16, 28, 31, 268, 264, 279, 280, 281, 282, 283 and 284. For instance, the CPSs used for prediction can include or consist of at least 4, 6, 8, 10, 12, 14, 16, 18 or 20 CPSs selected from the group.

[0540] In another preferred embodiment, the RCC disease genes used for predicting RCC and/or other solid tumors, such as prostate cancer and head/neck cancer, include or consist of one or more genes selected from the group consisting of CD44, CRADD, CCRL2, KIAA0837, KIAA0707, KIAA1113, EREG, UNK_AL050119, PPARD, CTSL, ATP2B1, UNK_AF052115, MITF, STAT3, KIAA0410, TPD52L2, UNK_AI732885, MARCO, LOC64116, and PDNP2. For instance, the RCC disease genes used for prediction can include or consist of at least 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 genes selected from the group.

[0541] In yet another preferred embodiment, the CPSs used for predicting RCC and/or other solid tumors, such as prostate cancer and head/neck cancer, include or consist of one or more CPSs selected from the group consisting of CPSs 17, 31, 37, 50, 59, 64, 69, 71, 264, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277 and 278. For instance, the CPSs used for prediction can include or consist of at least 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 CPSs selected from the group.

[0542] In one embodiment, the RCC disease genes used for predicting solid tumor versus solid tumor-free include or consist of one or more genes selected from the group consisting of NUMA1, CXCR4, IL10RA, M9, FAU, BRF2, RPS6, EEF1A2, BAG5, AKR1B1, UNK_AL022721, C1QBP, DKZP586E0820, NONO, PSMD3, UNK_N74607, UNK_AI743507, MAPKAPK5, and UNK_U79297. For instance, the RCC disease genes used for prediction can include or consist of at least 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 genes selected from the group.

[0543] In another embodiment, the CPSs used for predicting solid tumor versus solid tumor-free include or consist of one or more CPSs selected from the group consisting of CPSs 258, 285, 107, 286, 287, 256, 288, 255, 289, 259, 290, 266, 291, 292, 265, 131, 293, 294 and 295. For instance, the CPSs used for prediction can include or consist of at least 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 CPSs selected from the group.

[0544] Comparison of the expression profiles can also be performed based on a quantitative hybridization of arrayed DNA clones, the serial analysis of gene expression (SAGE) technology, or electronic analysis, such as the Transcript Imaging tool or the GEMTOOLS gene expression analysis program (Incyte Pharmaceuticals) or the GeneCalling and Quantitative Expression Analysis technology (Curagen). Algorithms, such as pattern recognition programs, can be used to compare the expression profiles of RCC disease genes with reference expression profiles.

E. RCC and Other Solid Tumor Prediction Based On Weighted Voting Algorithm

[0545] In accordance with one aspect of this invention, a weighted voting algorithm is used for comparing the expression profiles of a set of RCC disease genes in the human under diagnosis, to the expression profiles of the same set of RCC disease genes in disease-free humans and known RCC or solid tumor patients. The weighted voting algorithm is described in T.R. Golub, *et al.*, Science, 286: 531-537 (1999), and D.K. Slonim *et al.*, Procs. of the Fourth Annual International Conference on Computational Molecular Biology, Tokyo, Japan, April 8 - 11, p263-272 (2000). The algorithm can involve two-class or multi-class analysis. Multi-class analysis software, such as GeneCluster 2 software, is available from MIT Center for Genome Research at Whitehead Institute. The algorithm is capable of assigning the human under diagnosis to one of at least two classes.

[0546] Under one form of the algorithm, the human to be diagnosed is assigned to one of two classes (referred to as class 0 and class 1). For instance, class 0 may represent and consist of disease-free humans, and class 1 may represent and consist of RCC patients. A set of RCC disease genes are selected to create a class predictor (classifier). Each gene in the class predictor casts a weighted vote for one of the two classes (class 0 and class 1). The vote of gene "g" can be defined as $v_g = a_g (x_g - b_g)$, wherein $a_g = P(g, c)$ reflects the correlation between the expression level of gene "g" and the class distinction, $b_g = [x_0(g) +$

$x1(g)]/2$ is the average of the mean logs of the expression levels of gene "g" in class 0 and class 1, and x_g represents the normalized log of the expression level of gene "g" in the test sample. A positive v_g indicates a vote for class 0, and a negative v_g indicates a vote for class 1. $V0$ denotes the sum of all positive votes, and $V1$ denotes the absolute value of the sum of all negative votes. A prediction strength PS is defined as $PS = (V0 - V1)/(V0 + V1)$.

[0547] Cross-validation can be used to evaluate the accuracy of the class predictor created under the weighted voting algorithm. Briefly, one sample which has been used to identify the RCC disease genes under the neighborhood analysis is withheld. A class predictor is created based on the rest samples, and then used to predict the class of the sample withheld. This process can be repeated for each sample that has been used in the neighborhood analysis. Class predictors comprising different RCC disease genes can be evaluated using the cross-validation process, and the best class predictor with the most accurate predication can be identified. In addition, a suitable prediction strength (PS) threshold can be assessed by plotting the cumulative cross-validation error rate against the prediction strength.

[0548] In one embodiment, a positive predication that a test sample belongs to class 0 or class 1 can be made if the absolute value of PS for the test sample is no less than 0.3. Other PS threshold, such as no less than 0.1 or 0.2, can also be used.

[0549] In another embodiment, the class predictor or classifier consists of n RCC disease genes identified under the neighborhood analysis. A half of these RCC disease genes has the largest $P(g,c)$ scores, and the other half has the largest $-P(g,c)$ scores. The number n is the only free parameter in defining the class predictor.

[0550] Subsection G of this specification depicts detailed examples of building and training the RCC disease classifiers.

[0551] In a preferred embodiment, the class predictor comprises or consists of at least 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 genes selected from EEF1A2, TLR2, BRF2, LGALS3, SNRPG, DKFZP586E1621, NUMA1, SOD2, AKR1B1, DUSP6, SMARCE1, KIAA0669, MSF, IL1RN, PTMA, KIAA0410, PSMD3, T54, C1QBP, and OSR1. For instance, a 2-gene class predictor can consist of TLR2 and EEF1A2. A 4-gene class predictor can consist of TLR2, LGALS3, EEF1A2, and BRF2. A 6-gene class predictor can consist of TLR2, LGALS3, DKFZP586E1621, EEF1A2, BRF2, and SNRPG. An 8-gene class predictor can consist of TLR2, LGALS3, DKFZP586E1621, SOD2, EEF1A2, BRF2, SNRPG, and NUMA1. A 10-gene class predictor can consist of TLR2, LGALS3,

DKFZP586E1621, SOD2, DUSP6, EEF1A2, BRF2, SNRPG, NUMA1, and AKR1B1. A 12-gene class predictor can consist of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, and SMARCE1. A 14-gene class predictor can consist of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, and MSF. A 16-gene class predictor can consist of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, KIAA0410, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, MSF, and PTMA. An 18-gene class predictor can consist of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, KIAA0410, T54, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, MSF, PTMA, and PSMD3. Finally, a 20-gene class predictor consists of EEF1A2, TLR2, BRF2, LGALS3, SNRPG, DKFZP586E1621, NUMA1, SOD2, AKR1B1, DUSP6, SMARCE1, KIAA0669, MSF, IL1RN, PTMA, KIAA0410, PSMD3, T54, C1QBP, and OSR1.

[0552] In another preferred embodiment, the class predictor comprises (1) at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 genes selected from the group consisting of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, KIAA0410, T54 and OSR1, and (2) at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 genes selected from the group consisting of EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, MSF, PTMA, PSMD3 and C1QBP.

[0553] In yet another preferred embodiment, the class predictor comprises or consists of 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 genes selected from the group consisting of CD44, KIAA0410, MARCO, MAP3K8, NSP-CL, PIP5K1C, NRG1, RAB31, LGALS3, MEF2D, ITGA7, LHFPL2, ETS2, KHSRP, ENIGMA, UNK_AF038187, RAB13, TLR2, T54 and DUSP6.

[0554] In still another preferred embodiment, the class predictor comprises or consists of 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 genes selected from the group consisting of CD44, CRADD, CCRL2, KIAA0837, KIAA0707, KIAA1113, EREG, UNK_AL050119, PPARD, CTSL, ATP2B1, UNK_AF052115, MITF, STAT3, KIAA0410, TPD52L2, UNK_AI732885, MARCO, LOC64116, and PDNP2. The class predictors of this embodiment can be used to predict RCC, prostate cancer, head/neck cancer, and disease-free.

[0555] In still yet another preferred embodiment, the class predictor comprises or consists of 2, 4, 6, 8, 10, 12, 14, 16, 18 or 20 genes selected from the group consisting of

NUMA1, CXCR4, IL10RA, M9, FAU, BRF2, RPS6, EEF1A2, BAG5, AKR1B1, UNK_AL022721, C1QBP, DKZP586E0820, NONO, PSMD3, UNK_N74607, UNK_AI743507, MAPKAPK5, and UNK_U79297. The class predictors of this embodiment can be used to predict solid tumor versus solid tumor-free, regardless of the particular type of the solid tumor. The solid tumor predictable in this embodiment includes RCC, prostate cancer, and head/neck cancer.

[0556] In one embodiment, the reference expression levels of RCC disease genes, such as the expression levels derived from disease-free humans or known RCC or solid tumor patients, are stored in a database and are readily retrievable. In another embodiment, the comparison between expression profiles of various genes is performed electronically, such as using a computer system. The computer system comprises a processor coupled to a memory which stores data representing the expression profiles being compared. Preferably, the memory is readable as well as rewritable. The expression data stored in the memory can be changed, retrieved or otherwise manipulated. The memory also stores one or more programs capable of causing the processor to compare the stored expression profiles. For instance, the program may be able to execute a weighted voting algorithm. The processor can also be coupled to a polynucleotide array scanner and is capable of receiving signals from the scanner.

[0557] In another embodiment, a confidence threshold is established to optimize the accuracy of prediction and minimize the incidence of both false positive and false negative results. Average confidence scores collected for the accumulating pool of correctly diagnosed patients and correctly non-diagnosed disease-free individuals can be calculated and a reference range of values, for the particular predictive gene set diagnostic in question, can be reported.

F. Other Applications

[0558] The systematic gene expression analysis of this invention can be used to identify genes that are differentially expressed in peripheral blood samples isolated at different stages of the progression, development or treatment of RCC and/or other solid tumors. Genes thus-identified are molecular markers for monitoring the progression, development or treatment of RCC and/or other solid tumors. Genes thus-identified can also

be used as surrogate markers for evaluating the efficacy of a treatment for RCC or other solid tumors.

[0559] A clinical challenge concerning RCC and other solid tumors is the highly variable response of patients to therapy. The basic concept of pharmacogenomics is to understand a patient's genotype in relation to available treatment options and then individualize the most appropriate option for the patient. Different classes of RCC and/or other solid tumor patients can be created based on their different responses to a given therapy. Differentially expressed genes in these classes can be identified using the global gene expression analysis. Genes thus-identified can serve as predictive markers for forecasting whether a particular patient will be more or less responsive to the given therapy. For patients predicted to have a favorable outcome for the therapy, efforts to minimized toxicity of the therapy may be considered, whereas for those predicted not to respond to the therapy, treatment with other therapies or experimental regimes can be used.

[0560] The present invention also contemplates expression vectors encoding the RCC disease genes. The RCC disease genes may be under-expressed in RCC tumor cells. By introducing of the expression vectors into the patients, abnormal expression of the target genes may be corrected.

[0561] Suitable expression or gene delivery vectors are well known in the art. Preferably, these vectors are viral vectors, such as retroviral, lentiviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vectors. The viral vectors can also be astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vectors.

[0562] Delivery of the expression constructs is not limited to the above mentioned viral vectors. Other delivery methods can also be employed. These methods include nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus, ligand linked, gene guns, ionizing radiation, nucleic charge neutralization, or fusion with cell membranes. Naked DNA can also be employed. Exemplary methods to use naked DNA are known in the art. Uptake efficiency may be improved using biodegradable latex beads. This method can be further improved by treating the beads to increase their hydrophobicity. Liposome-based methods can also be used.

[0563] In addition, this invention contemplates expression vectors capable of expressing sequences that are anti-sense to a RCC disease gene of interest. The RCC disease gene of interest may be over-expressed in RCC or other solid tumor patients. By

introducing the antisense expression vector into these patients, the abnormal expression of the gene can be corrected.

[0564] An "antisense" polynucleotide comprises a nucleotide sequence which is complementary to a "sense" polynucleotide which encodes a protein. An antisense polynucleotide can bind via hydrogen bonds to the sense polynucleotide. The antisense polynucleotide can be complementary to an entire coding strand of the target gene, or a portion thereof. In one embodiment, the antisense polynucleotide molecule is antisense to a "noncoding region" in the coding strand of the target gene.

[0565] Antisense polynucleotides can be designed according to the rules of Watson and Crick base pairing. They may be oligonucleotides which are antisense to only a portion of the target gene. An antisense polynucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense polynucleotide can be constructed using chemical synthesis and enzymatic ligation reactions as appreciated by one of skill in the art. For example, an antisense polynucleotide (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense polynucleotides. Alternatively, the antisense polynucleotide can be produced biologically using an expression vector into which a polynucleotide has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted polynucleotide will be of an antisense orientation to the target polynucleotide of interest).

[0566] The antisense polynucleotides can be administered to a subject or applied *in situ* such that they hybridize or bind to cellular mRNAs and/or genomic DNAs of the target gene, thereby inhibiting the expression of the target gene. The hybridization can result in a stable duplex via conventional nucleotide complementarity. An example route for administering antisense polynucleotides includes direct injection at a tissue site. Antisense polynucleotides can also be modified first, and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface. Suitable modifications include linking the antisense polynucleotides to peptides or antibodies which bind to the cell surface receptors or antigens. In addition, the antisense polynucleotides can be delivered to cells using vectors. To achieve sufficient intracellular concentrations of the antisense molecules, strong pol II or pol III promoters may be used in the vectors.

[0567] In one embodiment, the antisense polynucleotides are α -anomeric polynucleotides. An α -anomeric polynucleotide molecule forms specific a double-stranded hybrid with a complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other. The antisense polynucleotide molecule can also comprise a 2'-o-methylribonucleotide or a chimeric RNA-DNA analogue.

[0568] In another embodiment, the antisense polynucleotide is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded polynucleotide, such as an mRNA, to which they have a complementary region. Thus, ribozymes can be used to catalytically cleave mRNA transcripts of the target gene in order to inhibit its expression. mRNAs transcribed from the target gene can be used to select from a pool of RNA molecules a catalytic RNA having a specific ribonuclease activity. Alternatively, the expression of the target gene can be inhibited by using nucleotide sequences complementary to the regulatory region (*e.g.*, the promoter and/or enhancers). These nucleotide sequences can form triple helical structures that prevent transcription of the gene in target cells.

[0569] Expression of the target gene can also be inhibited using RNA interference ("RNA_i"). This is a technique used in post transcriptional gene silencing ("PTGS"), in which the targeted gene activity is specifically abolished. RNA_i resembles in many aspects PTGS in plants and has been detected in many invertebrates including trypanosome, hydra, planaria, nematode and fruit fly (*Drosophila melanogaster*). It may be involved in the modulation of transposable element mobilization and antiviral state formation. RNA_i in mammalian systems is disclosed in PCT application WO00/63364. In one embodiment, dsRNA of at least about 21 nucleotides, homologous to the target gene, is introduced into cells.

[0570] Antibodies against the polypeptides encoded by the RCC disease genes can be also prepared and administered to patients in order to affect the function of the RCC disease genes. In one embodiment, the antibodies can reduce at least 25% of the activity of the target gene. Preferably, the antibodies reduce at least about 50% of the activity of the corresponding gene. Highly preferably, the antibodies reduce about 95-100% of the activity of the target gene.

[0571] A pharmaceutical composition comprising the antibody or expression vector of this invention can be made. The pharmaceutical composition also includes a pharmaceutically acceptable carrier. As used herein, a "pharmaceutically acceptable

carrier" is intended to include any and all solvents, solubilizers, fillers, stabilizers, binders, absorbents, bases, buffering agents, lubricants, controlled release vehicles, diluents, emulsifying agents, humectants, lubricants, dispersion media, coatings, antibacterial or antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well-known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary agents can also be incorporated into the compositions.

[0572] A pharmaceutical composition can be formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine; propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfate; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

[0573] Examples of suitable RCC disease genes that can be used as the targets of gene therapy or drug treatment include, but are not limited to, DUSP6, DRD2, ABL1, GUK1, MAP2K3, BSG, PPARG, TNNT1, ERN1, C4A, CCR1, PPARG, PDXK, MMP9, PPP3CB, CHRNA4, C8FW, PDNP2, ALDH5A1, and GPR12. Other examples include the RCC disease genes that are over- or under-expressed in both PBMCs and RCC tumor tissues.

[0574] In one embodiment, the present invention provides a kit comprising one or more polynucleotides, each of said one or more polynucleotides capable of hybridizing under stringent conditions to a gene selected from Gene-Table-4. Any primer/probe of this invention, or the complement thereof, can be included in the kit. The polynucleotide(s) can be labeled with fluorescent, radioactive, or other detectable moieties. In one instance, the one or more polynucleotides are contained in vials, tubes, bottles or other containing means.

In another instance, the one or more polynucleotides are stably attached to a solid support. Nucleic acid hybridization can be directly carried out on the solid support. In yet another instance, the kit contains at least 2, 3, 4, 5, 10, 15, 20, or more polynucleotides, each different polynucleotide capable of hybridizing under stringent conditions to a different respective gene selected from Gene-Table-4

[0575] In another embodiment, the kit of the present invention contains one or more antibodies capable of binding to the polypeptides encoded by the genes selected from Gene-Table-4. The antibodies can be labeled or unlabeled. Any antibody of this invention can be included in the kit. In one example, the kit also includes other immunodetection reagents, such as secondary antibodies, controls or enzyme substrates. In another example, the antibodies are included in one or more containers. In yet another example, the antibodies are stably bound to a solid support, such as a film, membrane, column matrix, or microtiter plate wells. Immunoassays can be performed directly on the solid support. In still yet another example, the kit contains at least 2, 3, 4, 5, 10, 15, 20, or more different antibodies, each different antibody capable of binding to a polypeptide encoded by a different respective genes selected from Gene-Table-4.

[0576] It should be understood that the above-described embodiments and the following examples are given by way of illustration, not limitation. Various changes and modifications within the scope of the present invention will become apparent to those skilled in the art from the present description.

G. Examples

Example 1. Isolation of RNA and Preparation of Labeled Microarray Targets

[0577] PBMCs from the clinical trials were isolated from whole blood samples (8mL) collected into CPT tubes according to the standard procedure. All disease-free and RCC blood samples were shipped or stored overnight prior to processing. PBMCs were purified over Ficoll gradients, washed two times with PBS and counted. Total RNA was isolated from PBMC pellets using the RNeasy mini kit (Qiagen, Valencia, CA). Labeled target for oligonucleotide arrays was prepared using a modification of the procedure described in Lockhart, *et al.*, Nature Biotechnology, 14: 1675-80 (1996). 2 µg total RNA was converted to cDNA by priming with an oligo-dT primer containing a T7 DNA

polymerase promoter at the 5' end. The cDNA was used as the template for *in vitro* transcription using a T7 DNA polymerase kit (Ambion, Woodlands, TX) and biotinylated CTP and UTP (Enzo). Labeled cRNA was fragmented in 40 mM Tris-acetate pH 8.0, 100 mM KOAc, 30 mM MgOAc for 35 minutes at 94°C in a final volume of 40 µl.

Example 2. Hybridization to Affymetrix Microarrays and Detection of Fluorescence

[0578] Individual RCC and disease-free samples were hybridized to HgU95A genechip (Affymetrix). No samples were pooled. 45 RCC patients and 20 disease-free volunteers were involved in the study. Tumors of the RCC patients were histopathologically classified as specific renal cell carcinoma subtypes using the Heidelberg classification of renal cell tumors described in Kovacs, *et al.*, J. Pathol., 183:131-133 (1997). Among the 45 RCC tumor samples, twenty-four samples were classified as conventional (clear cell) carcinomas, one sample was classified as granular, three samples were classified as papillary, seven samples were classified as mixed subtypes, and ten tumor samples were classified as unknown.

[0579] 10 µg of labeled target was diluted in 1x MES buffer with 100 µg/ml herring sperm DNA and 50 µg/ml acetylated BSA. To normalize arrays to each other and to estimate the sensitivity of the oligonucleotide arrays, *in vitro* synthesized transcripts of 11 bacterial genes were included in each hybridization reaction as described in Hill *et al.*, Science, 290: 809-812 (2000). The abundance of these transcripts ranged from 1:300,000 (3 ppm) to 1:1000 (1000 ppm) stated in terms of the number of control transcripts per total transcripts. As determined by the signal response from these control transcripts, the sensitivity of detection of the arrays ranged between about 1:300,000 and 1:100,000 copies/million. Labeled probes were denatured at 99°C for 5 minutes and then 45°C for 5 minutes and hybridized to oligonucleotide arrays comprised of over 12,500 human genes (HgU95A, Affymetrix). Arrays were hybridized for 16 hours at 45°C. The hybridization buffer was comprised of 100 mM MES, 1 M [Na⁺], 20 mM EDTA, and 0.01% Tween 20. After hybridization, the cartridges were washed extensively with wash buffer (6x SSPET), for instance, three 10-minute washes at room temperature. These hybridization and washing conditions are collectively referred to as "nucleic acid array hybridization conditions." The washed cartridges were then stained with phycoerythrin coupled to streptavidin.

[0580] 12x MES stock contains 1.22 M MES and 0.89 M $[\text{Na}^+]$. For 1000 ml, the stock can be prepared by mixing 70.4 g MES free acid monohydrate, 193.3 g MES sodium salt and 800 ml of molecular biology grade water, and adjusting volume to 1000 ml. The pH should be between 6.5 and 6.7. 2x hybridization buffer can be prepared by mixing 8.3 mL of 12x MES stock, 17.7 mL of 5 M NaCl, 4.0 mL of 0.5 M EDTA, 0.1 mL of 10% Tween 20 and 19.9 mL of water. 6x SSPET contains 0.9 M NaCl, 60 mM NaH_2PO_4 , 6 mM EDTA, pH 7.4, and 0.005% Triton X-100. In some cases, the wash buffer can be replaced with a more stringent wash buffer. 1000 ml stringent wash buffer can be prepared by mixing 83.3 mL of 12x MES stock, 5.2 mL of 5 M NaCl, 1.0 mL of 10% Tween 20 and 910.5 mL of water.

Example 3. Gene Expression Data Analysis

[0581] Data analysis was performed on raw fluorescent intensity values using GENECHIP 3.2 software (Affymetrix). GENECHIP 3.2 software uses an algorithm to calculate the likelihood as to whether a gene is "absent" or "present" as well as a specific hybridization intensity value or "average difference" for each transcript represented on the array. The algorithms used in these calculations are described in the Affymetrix GeneChip Analysis Suite User Guide (Affymetrix). The "average difference" for each transcript was normalized to "frequency" values according to the procedures of Hill *et al.*, Science, 290: 809-812 (2000). This was accomplished by referring the average difference values on each chip to a calibration curve constructed from the average difference values for the 11 control transcripts with known abundance that were spiked into each hybridization solution. This process also served to normalize between arrays.

[0582] Specific transcripts were evaluated further if they met the following criteria. First, genes that were designated "absent" by the GENECHIP 3.2 software in all samples were excluded from the analysis. Second, in comparisons of transcript levels between arrays, a gene was required to be present in at least one of the arrays. Third, for comparisons of transcript levels between groups, a Student's *t*-test was applied to identify a subset of transcripts that had a significant ($p < 0.05$) differences in frequency values. In certain cases, a fourth criterion, which requires that average fold changes in frequency values across the statistically significant subset of genes be 2-fold or greater, was also used.

[0583] Unsupervised hierarchical clustering of genes and/or arrays on the basis of similarity of their expression profiles was performed using the procedure described in Eisen, *et al.*, Proc. Nat. Acad. Sci., U.S.A., 95: 14863-14868 (1998). Nearest neighbor prediction analysis and supervised cluster analysis was performed using metrics illustrated in Golub *et al.*, Science, 286: 531-537 (1999). For hierarchical clustering and nearest neighbor prediction analysis, data were log transformed and normalized to have a mean value of zero and a variance of one. A Student's *t*-test was used to compare disease-free PBMC expression profiles to renal carcinoma PBMC profiles. In the comparisons, a *p* value < 0.05 was used to indicate statistical significance.

[0584] Expression profiles in various tissues can also be accessed and downloaded from the BioExpress database (GeneLogic, Gaithersburg MD). GeneLogic GX2000 software based analysis tools including fold change analysis and electronic northern analysis can be utilized to calculate fold changes and distribution of expression values, and expression profiles for different samples can be exported using the expression analysis tool for further analysis in the hierarchical clustering package (Eisen, *et al.*, Proc. Nat. Acad. Sci., U.S.A., 95: 14863-14868 (1998)).

[0585] A k-nearest neighbor's approach was used to perform a neighborhood analysis of real and randomly permuted data using a correlation metric ($P(g,c) = \mu_1 - \mu_2 / \sigma_1 + \sigma_2$) where *g* is the expression vector of a gene, *c* is the class vector, μ_1 and σ_1 define the mean expression level and standard deviation of the gene in class 1 and μ_2 and σ_2 define the mean expression level and standard deviation of the gene in class 2. The measures of correlation for the 246 most statistically significant upregulated genes of the true defined classes (RCC versus disease-free) were compared to the most statistically significant measures of correlation observed in randomly permuted class distinctions. The top 1%, 5% and median distance measurements of 100 randomly permuted classes compared to the observed distance measurements for RCC and disease-free classes are plotted. FIG. 1 depicts the statistical verification of the RCC disease genes identified in this invention.

Example 4. Identification of RCC Disease Genes in Peripheral Blood

[0586] Tables 6 and 7 list 184 RCC disease genes which are ranked by the number of samples in which the gene was called present (# Present). The *p*-value of the Student's *t*-test ("T-test (*p*-value)") for each of the 184 RCC disease genes is also listed in Table 6.

"Present" calls were calculated using GENECHIP 3.2 software by estimating whether a transcript was detected in a sample based on the strength of the gene's signal compared to background. See GeneChip® Expression Analysis Technical Manual, 701021 Rev.3 (1999-2002 Affymetrix, Inc.).

[0587] The "average difference" values for each transcript were normalized to "frequency" values using the scaled frequency normalization method in which the average differences for 11 control cRNAs with known abundance spiked into each hybridization solution were used to generate a global calibration curve. See Hill *et al.*, Genome Biol., 2(12):research0055.1-0055.13 (2001), which is incorporated herein in its entirety by reference. This calibration was then used to convert average difference values for all transcripts to frequency estimates, stated in units of parts per million (ppm) which can range, but are not limited to, from 1:300,000 (i.e., 3 ppm) to 1:1000 (1000 ppm).

[0588] Expression profiling analysis of the 20 disease-free PBMC RNA samples and 45 RCC PBMC RNA samples revealed that of the 12,626 transcripts on the HgU95A chip, 5,249 transcripts met the initial criteria for further analysis. The initial criteria were (1) there was at least one present call, and (2) at least one frequency was over 10 ppm. On average, 4023 transcripts were detected as "present" in the 45 RCC PBMCs, while 4254 expressed transcripts were detected as "present" in the 20 disease-free PBMCs.

[0589] The percent coefficients of variation (i.e., mean frequency / S.D. X 100) of each of the 5,249 original transcript levels across both groups of samples (45 RCC, 20 disease-free or normal PBMCs) were calculated (% COV). Transcripts were ranked where the least variable gene across the RCC samples received an RCC COV Rank =1 and the most variable gene across the RCC samples received an RCC COV Rank = 5249. This process was repeated for the 20 disease-free (normal) PBMC samples and the Normal COV Rank was calculated in similar fashion, i.e., the least variable gene across the disease-free RCC samples received an Norm COV Rank =1 and the most variable gene across the disease-free samples received an Norm COV Rank = 5249. In addition, fold changes were calculated as RCC Average Frequency / Normal Average Frequency, where a number equal to or greater than 2.0 was considered to represent a transcript induced in RCC PBMCs. Fold changes for each of the 5249 transcripts are depicted in Table 6. The number of samples possessing levels greater than 10ppm ("# Freq > 10") is also presented in Table 6 for each transcript. Moreover, the number of samples where the transcript was called present across the 45 RCC ("# Present RCC"), called present across the 20 Normals ("#

Present Normal”), present at levels greater than 10 ppm across the 45 RCC (“# Freq > 10 RCC”), and present at levels greater than 10 ppm across the 20 normals (“# Freq > 10 Norm”) are reported in Tables 6 and 7.

[0590] A fold change analysis and Student’s *t* test (two-tailed distribution; two-sample unequal variance) identified transcripts differentially expressed between RCC PBMCs and disease-free PBMCs. Transcript levels of the 184 RCC disease genes shown in Tables 6 and 7 differed on average by 2-fold or greater between disease-free and RCC PBMCs with an unadjusted p-value below 0.001 in a *t* test between the groups. Of these, 132 transcripts were expressed in at least 15% of the PBMC samples (present in 10 or more of the 65 profiles).

[0591] Furthermore, the possibility that the observed differences in expression profiles of CPT-purified RCC PBMC pellets and CPT-purified disease-free PBMC pellets were simply investigated. A correlation coefficient for each gene’s expression level with the level of granulocytes, lymphocytes and monocytes measured in PBMC samples was calculated. The relative correlation of expression of each gene with the level of each cell type was ranked to determine whether the disease-associated transcripts detected in RCC PBMCs were over-represented in a given cell population. The relative rank (out of the 5,249 transcripts passing the initial data filter) correlations of each transcript with the absolute numbers of granulocytes, lymphocytes and monocytes measured in PBMC samples were obtained. These analyses indicate that the vast majority of disease-associated transcripts identified in PBMCs of RCC patients were not simply correlated with specific cell subpopulations in peripheral blood.

[0592] An initial unsupervised cluster analysis approach which hierarchically groups samples and genes based on correlation coefficients (Eisen *et al.*, *supra*) was performed using the 5,249 transcripts passing the initial filtering criteria. FIG. 2 depicts a dendrogram of sample relatedness using expressed gene expression values. RCC patient PBMC expression profiles were denoted by white bars and disease-free volunteer PBMC expression profiles were indicated by black bars. The dendrogram grouped the majority of RCC PBMCs (42/45) into a single RCC-specific cluster while expression patterns of disease-free PBMCs and a small subset of RCC PBMCs (3/45) formed a separate cluster.

[0593] Among the 184 RCC disease genes listed in Tables 6a and 7, there were several inflammatory-related genes, including Toll-like receptor 2, galectin-3, IL-1 receptor antagonist, and aquaporin-9, a water channel implicated in leukocyte migration. The

unchanged levels of many other cytokines, chemokines and their respective receptors between normal and RCC PBMCs suggest that a specific, rather than global, activation of PBMCs constituted part of the disease signature in RCC peripheral blood.

[0594] A substantial number of the transcripts detected as significantly changed in PBMCs from RCC patients possess a significant degree of variability across the RCC PBMC profiles. This indicates that while the levels of these transcripts were significantly distinct from levels in normal PBMCs, there was relative heterogeneity of expression of these transcripts across RCC patients. It will be of great interest to determine whether any of these disease-associated yet significantly variable transcripts in RCC PBMCs will be correlated with any clinical categories of response, once clinical indices of outcome and follow-up are satisfactorily measured in these patients.

Table 6. 184 DISEASE-ASSOCIATED TRANSCRIPTS IN RCC PATIENTS

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
AF051152	toll-like receptor 2	Hs.63668	3753	2841	2.5	4.824E-10	65	61
AB006780	lectin, galactoside-binding, soluble, 3 (galectin 3)	Hs.621	3123	2648	2.1	2.373E-09	65	65
AF032886	forkhead box O3A	Hs.14845	4751	2553	2.9	1.823E-07	65	63
M64925	membrane protein, palmitoylated 1 (55kD)	Hs.1861	4885	3740	3.4	2.921E-07	65	65
X12451	cathepsin L	Hs.78056	4948	4959	3.5	1.053E-06	65	64
D32143	biliverdin reductase B (flavin reductase (NADPH))	Hs.76289	4978	4946	3.8	1.176E-06	65	51
AF079221	BCL2/adenovirus E1B 19kD-interacting protein 3-like	Hs.132955	4973	738	3.4	1.667E-06	65	65
L76200	guanylate kinase 1	Hs.3764	4702	545	2.3	2.341E-06	65	65
M25915	clusterin (complement lysis inhibitor, SP-40, testosterone-repressed prostate message 2, apolipoprotein J)	Hs.75106	4671	2556	2.2	5.682E-06	65	65
X12496	glycophorin C (Gerbich blood group)	Hs.81994	4784	2756	2.3	8.074E-06	65	65
L07648	MAX-interacting protein 1	Hs.118630	5017	3607	3.1	1.054E-05	65	65
M24069	cold shock domain protein A	Hs.198726	5080	1964	4.3	1.214E-05	65	62
L07648	MAX-interacting protein 1	Hs.118630	4993	1677	2.7	1.961E-05	65	65
D14874	adrenomedullin	Hs.394	4945	4139	2.5	2.328E-05	65	64
AL050254	F-box protein 7	Hs.5912	4969	39	2.3	4.875E-05	65	65
X17644	G1 to S phase transition 1	Hs.2707	5068	1732	2.8	0.0001073	65	44
AI565760	ganglioside expression factor 2	Hs.6518	4966	527	2.2	0.0001082	65	65
V00505	hemoglobin, delta	Hs.36977	5167	5070	6.4	0.0001176	65	58
X79535	tubulin, beta polypeptide	Hs.336780	4836	4393	2.0	0.0001308	65	41
U76248	seven in absentia (Drosophila)	Hs.20191	4982	395	2.1	0.0001703	65	62

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
	homolog 2							
AB013382	dual specificity phosphatase 6	Hs.180383	4363	4916	3.2	2.665E-09	64	44
AF025533	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Hs.105928	4281	3711	2.3	1.796E-07	64	62
U05770	annexin A5	Hs.300711	3405	4405	2.1	1.998E-07	64	54
X60364	aminolevulinate, delta-, synthase 2 (sideroblastic/hypochromic anemia)	Hs.323383	5066	4919	6.8	7.041E-07	64	65
AF001461	core promoter element binding protein	Hs.285313	3489	5175	2.2	2.229E-05	64	62
Z35491	BCL2-associated athanogene	Hs.41714	5040	1910	2.6	8.933E-05	64	63
D83664	S100 calcium-binding protein A12 (calgranulin C)	Hs.19413	5048	4905	2.3	0.0005046	64	50
L19185	thioredoxin-dependent peroxide reductase 1 (thiol-specific antioxidant 1, natural killer- enhancing factor B)	Hs.146354	5130	4840	3.0	0.0005744	64	35
M24470	guanosine monophosphate reductase	Hs.1435	5095	4312	2.6	0.0006112	64	47
X97324	adipose differentiation-related protein; adipophilin	Hs.3416	5170	2819	3.6	0.0009168	64	64
X52015	interleukin 1 receptor antagonist	Hs.81134	4900	5136	4.1	1.249E-07	63	59
AB008775	aquaporin 9	Hs.104624	4467	4955	2.5	6.609E-07	63	39
J02973	thrombomodulin	Hs.2030	4665	5035	2.1	6.829E-05	63	57
D87116	mitogen-activated protein kinase kinase 3	Hs.180533	4377	4016	2.1	1.391E-06	62	65
N74607	ESTs, Highly similar to	Hs.234642	4662	4739	0.4	0.0001043	62	50

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
	AQUAPORIN 3 [H.sapiens]							
M36820	GRO2 oncogene	Hs.75765	5077	5213	3.0	0.0002266	62	46
M38690	CD9 antigen (p24)	Hs.1244	4838	5074	2.0	0.0005439	62	26
X90999	hydroxyacyl glutathione hydrolase; glyoxalase 2	Hs.155482	5138	4356	4.3	0.0001189	61	35
M94856	fatty acid binding protein 5 (psoriasis-associated)	Hs.153179	4992	5080	3.4	4.231E-06	60	31
Z32684	Kell blood group precursor (McLeod phenotype)	Hs.78919	4994	2026	3.0	7.435E-06	60	22
AF061034	tumor necrosis factor alpha- inducible protein with leucine zipper domains; Huntingtin interacting protein L	Hs.278898	4937	1223	2.5	1.229E-05	60	13
J04102	v-ets avian erythroblastosis virus E26 oncogene homolog 2	Hs.85146	4668	4364	2.1	2.14E-05	60	27
L42542	ralA binding protein 1	Hs.75447	4795	3443	2.0	6.245E-05	60	17
AF141349	Tubulin, Beta		4864	5013	2.3	6.903E-05	60	29
D38583	S100 calcium-binding protein A11 (calgizarin)	Hs.256290	4942	5084	2.4	0.0001294	60	45
X04327	2,3-bisphosphoglycerate mutase	Hs.198365	5156	2762	3.4	0.0005919	60	19
J04027	ATPase, Ca++ transporting, plasma membrane 1	Hs.78546	4590	4932	2.3	4.802E-06	59	38
AF141349	Tubulin, Beta	Hs.336780	5011	4590	2.5	8.725E-05	59	34
Y00630	plasminogen activator inhibitor, type II (arginine-serpin)	Hs.75716	5022	5214	2.7	0.0001986	59	59
U29091	selenium binding protein 1	Hs.334841	5123	5032	6.9	1.249E-05	58	59
U28389	erythrocyte membrane protein band 4.9 (dematin)	Hs.274122	5102	3910	4.0	3.927E-05	58	65
X64364	basigin	Hs.74631	5093	1296	3.6	5.217E-05	58	53
X00737	nucleoside phosphorylase	Hs.75514	4507	5038	2.0	0.0001001	58	39

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
M26683	small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je)	Hs.303649	5139	5215	6.6	3.159E-05	57	49
AI349593	hemoglobin, epsilon 1	Hs.117848	5064	5121	3.0	8.566E-05	56	13
L22075	guanine nucleotide binding protein (G protein), alpha 13	Hs.1666	3815	4953	2.2	1.35E-06	53	20
AA135683	brain acid-soluble protein 1	Hs.79516	4198	4148	2.1	1.44E-06	53	32
U00672	interleukin 10 receptor, alpha	Hs.327	4277	4086	0.5	4.823E-05	53	54
AL080235	DKFZP586E1621 protein	Hs.35861	4889	3240	3.0	1.13E-06	52	23
K00650	v-fos FBJ murine osteosarcoma viral oncogene homolog	Hs.25647	5101	4029	0.5	0.0001975	52	55
M28225	small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je)	Hs.303649	5155	5197	6.7	5.68E-05	51	37
S78798	Cluster Incl S78798: 1- phosphatidylinositol-4- phosphate 5-kinase isoform C [human, PBLs, mRNA, 1835 nt].	Hs.108966	4875	665	2.5	4.123E-06	50	10
AL049963	Homo sapiens mRNA; cDNA DKFZp564A132 (from clone DKFZp564A132)	Hs.284205	4651	4155	2.2	6.76E-06	50	18
L22005	cell division cycle 34	Hs.76932	5082	4185	3.5	4.315E-05	50	29
K02401	chorionic somatomammotropin hormone 1 (placental lactogen)		4673	4930	0.4	0.000423	50	36
X14787	thrombospondin 1	Hs.87409	5001	5217	2.4	0.0004915	50	49
X75042	v-rel avian reticuloendotheliosis viral oncogene homolog	Hs.44313	2993	4933	2.3	5.819E-08	49	13
AA131149	S100 calcium-binding protein P	Hs.2962	4970	5115	2.4	0.0001709	49	35
M35999	integrin, beta 3 (platelet)	Hs.87149	4908	4341	2.6	1.011E-05	48	23

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
	glycoprotein IIIa, antigen CD61)							
U21049	epithelial protein up-regulated in carcinoma, membrane associated protein 17	Hs.271473	4932	3123	2.3	3.94E-05	48	31
M19267	tropomyosin 1 (alpha)	Hs.77899	4904	2893	2.3	2E-05	47	11
M27819	solute carrier family 4, anion exchanger, member 1	Hs.185923	5134	5216	7.5	1.725E-05	46	42
M27492	interleukin 1 receptor, type I	Hs.82112	4888	5142	2.4	9.826E-05	46	25
X07834	superoxide dismutase 2, mitochondrial	Hs.372783	4867	2075	2.5	3.956E-06	45	17
X72308	small inducible cytokine A7 (monocyte chemotactic protein 3)	Hs.251526	5075	5097	3.6	3.391E-05	45	26
AI679353	ESTs, Weakly similar to !!!! ALU CLASS E WARNING ENTRY !!!! [H.sapiens]	Hs.182611	5003	5154	2.5	0.0001701	45	14
L42243	interferon (alpha, beta and omega) receptor 2	Hs.173936	4415	3824	2.1	2.471E-06	44	13
D10925	chemokine (C-C motif) receptor 1	Hs.301921	4811	4666	2.5	5.121E-06	44	13
D30783	epiregulin	Hs.115263	4998	3590	3.1	5.694E-06	44	18
S77763	nuclear factor (erythroid- derived 2), 45kD	Hs.75643	5124	2980	3.2	0.0002806	42	12
X79535	tubulin, beta polypeptide		4780	5120	2.6	5.817E-06	41	42
U61836	Human putative cyclin G1 interacting protein mRNA, partial sequence	Hs.92374	4788	4609	2.4	8.146E-06	41	14
M34480	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B)	Hs.785	5029	5006	3.1	2.414E-05	39	30

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
M63835	Fc fragment of IgG, high affinity Ia, receptor for (CD64)	Hs.77424	4809	4285	2.1	3.916E-05	39	11
AF017257	v-ets avian erythroblastosis virus E26 oncogene homolog 2		3987	897	2.1	3.459E-08	38	5
AA527880	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18)	Hs.661	5081	4675	3.7	3.306E-05	37	28
AF065389	tetraspan 5	Hs.20709	5021	953	2.4	8.816E-05	37	11
D86961	lipoma HMGIC fusion partner- like 2	Hs.79299	4939	2043	3.7	3.534E-07	35	12
U61836	Human putative cyclin G1 interacting protein mRNA, partial sequence	Hs.92374	5119	5156	4.2	7.33E-05	35	17
AF026939	interferon-induced protein with tetratricopeptide repeats 4	Hs.181874	4750	4395	2.1	4.978E-05	34	14
M25322	selectin P (granule membrane protein 140kD, antigen CD62)	Hs.73800	5133	2402	3.1	0.0004767	33	15
AB007943	KIAA0474 gene product	Hs.75151	5057	4196	3.3	2.149E-05	30	65
M60298	erythrocyte membrane protein band 4.2	Hs.733	5179	3017	5.6	0.0003742	30	17
X58851	myosin, light polypeptide 4, alkali; atrial, embryonic	Hs.356717	5151	3371	4.0	0.0002666	29	12
J05070	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	Hs.151738	4778	2918	2.3	4.644E-06	28	6
U43774	Fc fragment of IgA, receptor for	Hs.193122	4777	4857	2.4	9.317E-06	27	10
AF052111	Homo sapiens clone 23953 mRNA sequence	Hs.21334	4215	3789	2.2	2.807E-07	26	2
AA187563	ESTs, Highly similar to CGI-56 protein [H.sapiens]	Hs.8836	4478	1311	2.2	3.825E-07	26	7

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
H12458	y12d03.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148517 3' similar to WNT6		4250	4652	2.1	4.07E-06	26	57
Z23115	BCL2-like 1	Hs.305890	5086	5167	4.3	2.221E-05	26	22
U12471	Human thrombospondin-1 gene, partial cds	Hs.87409	5041	5030	2.9	5.46E-05	26	18
L06895 *	MAX dimerization protein	Hs.109012	4985	3015	2.3	8.798E-05	26	6
AB023211	peptidyl arginine deiminase, type II	Hs.33455	4936	4868	2.3	9.707E-05	26	8
D63940	MAX-interacting protein 1	Hs.118630	5114	1391	3.9	7.286E-05	25	10
X74039	plasminogen activator, urokinase receptor	Hs.179657	5033	2574	2.8	4.169E-05	24	7
AB018293	KIAA0750 gene product	Hs.314434	5163	4386	4.9	0.0001921	24	17
AA978353	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	Hs.374464	3351	1336	2.1	1.947E-09	23	3
AJ243797	three prime repair exonuclease 1	Hs.278408	4915	5202	3.2	4.017E-06	23	15
U89606	pyridoxal (pyridoxine, vitamin B6) kinase	Hs.38041	5046	3734	2.4	0.0002111	23	8
M19267	tropomyosin 1 (alpha)	Hs.77899	4274	771	2.1	3.017E-07	22	8
L35240	enigma (LIM domain protein)	Hs.102948	3575	2807	2.1	3.028E-08	21	12
AL096737	Homo sapiens mRNA; cDNA DKFZp434F152 (from clone DKFZp434F152)	Hs.5167	4814	4749	2.6	3.048E-06	19	64
D14689	nucleoporin 214kD (CAIN)	Hs.170285	4623	4524	2.2	6.273E-06	19	46
U36341	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Hs.187958	5032	3765	2.7	6.494E-05	19	28

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
M77016	tropomodulin	Hs.170453	5186	2442	4.9	0.0007758	19	11
U91316	cytosolic acyl coenzyme A thioester hydrolase	Hs.8679	4502	2737	2.1	1.898E-06	18	12
M62896	Human lipocortin (LIP) 2 pseudogene mRNA, complete cds-like region	Hs.348252	3841	3722	2.0	3.217E-07	17	4
L40904	peroxisome proliferative activated receptor, gamma	Hs.100724	5141	4460	6.1	4.033E-05	16	20
U66359	T54 protein	Hs.100391	4764	2450	4.3	5.444E-09	15	13
W28931	ESTs, Weakly similar to 38kDa splicing factor [H.sapiens]	Hs.283976	4933	5232	4.0	1.143E-06	15	29
AB006537	interleukin 1 receptor accessory protein	Hs.173880	4072	1425	2.1	5.561E-08	13	1
U97067	Cluster Incl U97067: Homo sapiens alpha-catenin-like protein mRNA, complete cds.	Hs.58488	4819	4961	2.3	2.571E-05	13	6
U19599	BCL2-associated X protein	Hs.159428	4039	4061	0.5	5.153E-05	13	6
AA628946	KH-type splicing regulatory protein (FUSE-binding protein 2)	Hs.91142	3189	4910	2.5	5.017E-09	12	44
AI961220	serine protease inhibitor, Kazal type 1	Hs.181286	5035	2667	2.8	4.079E-05	12	4
AL049250	Homo sapiens mRNA; cDNA DKFZp564D113 (from clone DKFZp564D113)	Hs.356390	5027	3940	2.3	0.0002155	12	5
AL031230	aldehyde dehydrogenase 5 family, member A1 (succinate- semialdehyde dehydrogenase)		4830	1089	2.3	6.562E-06	11	3
U68111	protein phosphatase 1; regulatory (inhibitor) subunit 2		4983	5109	3.0	1.282E-05	11	19
AF035819	macrophage receptor with	Hs.67726	4726	1966	2.6	4.175E-07	10	5

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
	collagenous structure							
AJ000480	phosphoprotein regulated by mitogenic pathways	Hs.7837	4716	2979	2.2	5.308E-06	10	5
U58917	interleukin 17 receptor	Hs.129751	4674	2850	2.0	1.796E-05	10	1
X90857	Conserved gene telomeric to alpha globin cluster	Hs.19699	5074	2410	2.5	0.0003808	10	13
J05500	spectrin, beta, erythrocytic (includes sperocytosis, clinical type I)	Hs.47431	5122	4713	5.5	2.364E-05	9	17
X54412	collagen, type IX, alpha 1	Hs.154850	5013	5050	2.5	0.0001267	9	28
X75593	RAB13, member RAS oncogene family	Hs.151536	4147	2502	2.3	2.116E-08	8	13
D38037	FK506-binding protein 1B (12.6 kD)	Hs.77643	4886	4835	2.2	0.0001298	8	2
J02854	myosin regulatory light chain 2, smooth muscle isoform	Hs.9615	5111	1099	3.3	0.0001603	8	7
AF034209	RIG-like 5-6	Hs.166175	5042	3640	2.2	0.0004712	8	4
U24578	complement component 4A		5108	4896	2.7	0.0007918	8	15
AB011161	phosphatidylinositol-4- phosphate 5-kinase, type I, gamma	Hs.275182	4546	4539	2.9	3.707E-08	7	24
L23959	transcription factor Dp-1	Hs.79353	4621	1087	2.0	8.135E-06	7	2
M64788	RAP1, GTPase activating protein 1	Hs.75151	5153	1951	3.5	0.0004775	7	10
X51362	dopamine receptor D2	Hs.73893	4781	5203	3.4	4.287E-07	6	21
AB000520	adaptor protein with pleckstrin homology and src homology 2 domains	Hs.105052	4462	1941	2.2	7.021E-07	6	3
U43843	Neuro-d4 (rat) homolog	Hs.159589	4124	4902	2.1	5.029E-06	6	5
D43642	transcription factor-like 1	Hs.2430	3926	4299	2.3	4.473E-08	5	35

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
W26700	ESTs, Highly similar to brain specific Na ⁺ -dependent inorganic phosphate cotransporter [R.norvegicus]	Hs.6535	3942	4297	2.2	2.112E-07	5	5
AA844998	pancreatic polypeptide	Hs.184604	4324	4714	2.3	5.173E-07	5	11
AJ223948	RNA helicase family	Hs.48295	5034	1093	2.4	0.0001437	5	3
AJ000644	speckle-type POZ protein	Hs.129951	4924	2873	2.0	0.0001677	5	4
W27095	B7 protein	Hs.155586	4896	4612	0.5	0.0005773	5	29
AF032108	integrin, alpha 7	Hs.74369	3875	2021	2.0	8.428E-08	4	1
M13207	colony stimulating factor 2 (granulocyte-macrophage)	Hs.1349	4803	3030	2.9	3.338E-07	4	7
AF059202	diacylglycerol O- acyltransferase (mouse) homolog	Hs.288627	4782	4723	2.6	2.08E-06	4	10
X82460	hydroxyprostaglandin dehydrogenase 15-(NAD)	Hs.77348	4818	4170	2.3	1.647E-05	4	3
AJ011712	troponin T1, skeletal, slow	Hs.73980	4935	1426	2.0	0.0001917	4	2
L37127	polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Hs.80475	5104	1098	2.9	0.0002842	4	5
AF089814	tumor suppressor deleted in oral cancer-related 1	Hs.355753	5038	2134	2.2	0.0003873	4	2
L07592	peroxisome proliferative activated receptor, delta	Hs.106415	4163	4744	2.4	9.857E-08	3	18
AB020644	long fatty acyl-CoA synthetase 2 gene	Hs.14945	4424	4306	2.0	7.813E-06	3	4
AF068706	adaptor-related protein complex 1, gamma 2 subunit	Hs.343244	5113	1688	4.1	5.554E-05	3	12
AF059198	ER to nucleus signalling 1	Hs.137575	4683	5101	2.1	0.0001249	3	17
AF055027	coactivator-associated arginine	Hs.143696	4999	2921	2.1	0.0002883	3	6

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
	methyltransferase-1							
L03785	myosin, light polypeptide 5, regulatory	Hs.170482	5154	3757	3.0	0.0009999	3	8
X91348	putative non-coding transcript (DiGeorge critical region 5)	Hs.335328	3774	2545	2.1	2.892E-08	2	1
L32831	G protein-coupled receptor 3	Hs.66542	4578	5177	2.6	3.18E-06	2	18
AI732885	Human BRCA2 region, mRNA sequence CG011	Hs.142907	4892	681	2.1	4.626E-05	2	2
U96919	inositol polyphosphate-4- phosphatase, type I, 107kD	Hs.32944	5118	3038	3.2	0.0002322	2	7
U62433	cholinergic receptor, nicotinic, alpha polypeptide 4	Hs.10734	5089	5189	2.8	0.0004996	2	9
AF055000	H.sapiens mRNA for unknown liver orphan	Hs.118463	4378	3305	2.5	5.537E-08	1	58
J05581	mucin 1, transmembrane	Hs.89603	4634	4942	2.7	4.138E-07	1	10
U48213	D site of albumin promoter (albumin D-box) binding protein	Hs.155402	4812	3542	0.4	1.723E-06	1	32
D45421	phosphodiesterase I/nucleotide pyrophosphatase 2 (autotaxin)	Hs.174185	4753	2549	2.4	2.976E-06	1	4
AF017786	Phosphatidic acid phosphatase type 2b	Hs.173717	4679	680	2.1	5.747E-06	1	3
AB010419	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	Hs.110099	5065	3641	3.4	2.068E-05	1	11
AF070587	Homo sapiens clone 24741 mRNA sequence	Hs.25770	4869	4801	2.2	6.352E-05	1	13
AJ001481	double homeobox, 1	Hs.274469	5004	2922	2.5	6.436E-05	1	7
U70732	glutamic-pyruvate transaminase (alanine aminotransferase)	Hs.103502	4512	5163	2.1	0.000245	1	24

GenBank Accession Number	Gene Annotation	Unigene ID	RCC COV Rank	Norm COV Rank	Fold Change	T-test (p-value)	# Present	# Freq>10
AF038171	Cluster Incl AF038171: Homo sapiens clone 23671 mRNA sequence.		5059	1096	2.3	0.0002938	1	3
AF070629	RAB2, member RAS oncogene family	Hs.78305	5020	1967	2.1	0.0003503	1	3
L17330	pre-T/NK cell associated protein	Hs.280	5044	1094	2.2	0.0003682	1	3
AI077476	KIAA0353 protein	Hs.10587	5053	3147	2.3	0.0004087	1	7
AF054185	proteasome (prosome, macropain) subunit, alpha type, 7	Hs.233952	4963	5009	2.1	0.0005972	1	15
U18548	G protein-coupled receptor 12	Hs.123034	5062	1097	2.1	0.0008125	1	2

Table 7. 184 DISEASE-ASSOCIATED TRANSCRIPTS IN RCC PATIENTS

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
AF051152	toll-like receptor 2	45	20	45	16	Activated T Cells
AB006780	lectin, galactoside-binding, soluble, 3 (galectin 3)	45	20	45	20	
AF032886	forkhead box O3A	45	20	45	18	
M64925	membrane protein, palmitoylated 1 (55kD)	45	20	45	20	
X12451	cathepsin L	45	20	45	19	Activated T Cells
D32143	biliverdin reductase B (flavin)	45	20	44	7	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
	reductase (NADPH))					
AF079221	BCL2/adenovirus E1B 19kD- interacting protein 3-like	45	20	45	20	
L76200	guanylate kinase 1	45	20	45	20	
M25915	clusterin (complement lysis inhibitor, SP-40, testosterone- repressed prostate message 2, apolipoprotein J)	45	20	45	20	
X12496	glycophorin C (Gerbich blood group)	45	20	45	20	
L07648	MAX-interacting protein 1	45	20	45	20	
M24069	cold shock domain protein A	45	20	45	17	
L07648	MAX-interacting protein 1	45	20	45	20	
D14874	adrenomedullin	45	20	45	19	
AL050254	F-box protein 7	45	20	45	20	
X17644	G1 to S phase transition 1	45	20	35	9	Activated T Cells
AI565760	ganglioside expression factor 2	45	20	45	20	
V00505	hemoglobin, delta	45	20	43	15	Renal failure
X79535	tubulin, beta polypeptide	45	20	34	7	
U76248	seven in absentia (Drosophila) homolog 2	45	20	43	19	
AB013382	dual specificity phosphatase 6	45	19	40	4	
AF025533	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	44	20	44	18	
U05770	annexin A5	45	19	43	11	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
X60364	aminolevulinate, delta- synthase 2 (sideroblastic/hypochromic anemia)	45	19	45	20	Renal failure
AF001461	core promoter element binding protein	45	19	45	17	
Z35491	BCL2-associated athanogene	44	20	44	19	
D83664	S100 calcium-binding protein A12 (calgranulin C)	44	20	37	13	
L19185	thioredoxin-dependent peroxide reductase 1 (thiol-specific antioxidant 1, natural killer- enhancing factor B)	45	19	31	4	
M24470	guanosine monophosphate reductase	44	20	34	13	
X97324	adipose differentiation-related protein; adipophilin	44	20	44	20	
X52015	interleukin 1 receptor antagonist	44	19	44	15	Activated T Cells
AB008775	aquaporin 9	44	19	33	6	
J02973	thrombomodulin	44	19	43	14	
D87116	mitogen-activated protein kinase kinase 3	44	18	45	20	
N74607	ESTs, Highly similar to AQUAPORIN 3 [H.sapiens]	42	20	30	20	Activated T Cells
M36820	GRO2 oncogene	43	19	36	10	
M38690	CD9 antigen (p24)	44	18	23	3	
X90999	hydroxyacyl glutathione	44	17	31	4	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
	hydrolase; glyoxalase 2					
M94856	fatty acid binding protein 5 (psoriasis-associated)	42	18	28	3	Activated T Cells
Z32684	Kell blood group precursor (McLeod phenotype)	41	19	22	0	
AF061034	tumor necrosis factor alpha- inducible protein with leucine zipper domains; Huntingtin interacting protein L	44	16	13	0	
J04102	v-ets avian erythroblastosis virus E26 oncogene homolog 2	41	19	25	2	
L42542	ralA binding protein 1	42	18	17	0	
AF141349	Tubulin, Beta	43	17	25	4	Activated T Cells
D38583	S100 calcium-binding protein A11 (calgizarin)	40	20	33	12	
X04327	2,3-bisphosphoglycerate mutase	42	18	18	1	
J04027	ATPase, Ca++ transporting, plasma membrane 1	43	16	33	5	
AF141349	Tubulin, Beta	43	16	29	5	Activated T Cells
Y00630	plasminogen activator inhibitor, type II (arginine-serpin)	41	18	42	17	
U29091	selenium binding protein 1	44	14	44	15	
U28389	erythrocyte membrane protein band 4.9 (deniatin)	43	15	45	20	
X64364	basigin	43	15	43	10	
X00737	nucleoside phosphorylase	43	15	34	5	Activated T

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with Cells
M26683	small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je)	40	17	37	12	
A1349593	hemoglobin, epsilon 1	42	14	13	0	
L22075	guanine nucleotide binding protein (G protein), alpha 13	41	12	19	1	
AA135683	brain acid-soluble protein 1	39	14	29	3	
U00672	interleukin 10 receptor, alpha	33	20	34	20	
AL080235	DKFZP586E1621 protein	41	11	23	0	
K00650	v-fos FBJ murine osteosarcoma viral oncogene homolog	32	20	35	20	Activated T Cells
M28225	small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je)	36	15	34	3	
S78798	Cluster Incl S78798: 1- phosphatidylinositol-4- phosphate 5-kinase isoform C [human, PBLs, mRNA, 1835 nt].	39	11	10	0	
AL049963	Homo sapiens mRNA; cDNA DKFZp564A132 (from clone DKFZp564A132)	38	12	17	1	Renal failure
L22005	cell division cycle 34	38	12	27	2	
K02401	chorionic somatomammotropin hormone 1 (placental lactogen)	30	20	17	19	
X14787	thrombospondin 1	38	12	39	10	
X75042	v-rel avian reticuloendotheliosis	35	14	12	1	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
	viral oncogene homolog					
AA131149	S100 calcium-binding protein P	35	14	30	5	
M35999	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	36	12	22	1	
U21049	epithelial protein up-regulated in carcinoma, membrane associated protein 17	37	11	28	3	
M19267	tropomyosin 1 (alpha)	36	11	11	0	
M27819	solute carrier family 4, anion exchanger, member 1	40	6	40	2	Renal failure
M27492	interleukin 1 receptor, type I	36	10	21	4	Activated T Cells
X07834	superoxide dismutase 2, mitochondrial	36	9	17	0	
X72308	small inducible cytokine A7 (monocyte chemotactic protein 3)	35	10	24	2	
AI679353	ESTs, Weakly similar to !!!! ALU CLASS E WARNING ENTRY !!!! [H.sapiens]	37	8	13	1	
L42243	interferon (alpha, beta and omega) receptor 2	36	8	13	0	
D10925	chemokine (C-C motif) receptor 1	35	9	13	0	
D30783	epiregulin	35	9	18	0	
S77763	nuclear factor (erythroid- derived 2), 45kD	36	6	12	0	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
X79535	tubulin, beta polypeptide	33	8	36	6	Renal failure & Activated T Cells
U61836	Human putative cyclin G1 interacting protein mRNA, partial sequence	33	8	14	0	
M34480	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B)	33	6	27	3	
M63835	Fc fragment of IgG, high affinity Ia, receptor for (CD64)	28	11	11	0	
AF017257	v-ets avian erythroblastosis virus E26 oncogene homolog 2	32	6	5	0	
AA527880	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (18kD, B18)	24	13	26	2	Renal failure
AF065389	tetraspan 5	29	8	11	0	
D86961	lipoma HMGIC fusion partner- like 2	31	4	12	0	Renal failure
U61836	Human putative cyclin G1 interacting protein mRNA, partial sequence	29	6	16	1	
AF026939	interferon-induced protein with tetra-trico-peptide repeats 4	25	9	14	0	
M25322	selectin P (granule membrane protein 140kD, antigen CD62)	27	6	15	0	
AB007943	KIAA0474 gene product	24	6	45	20	
M60298	erythrocyte membrane protein	28	2	17	0	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
	band 4.2					
X58851	myosin, light polypeptide 4, alkali; atrial, embryonic	26	3	12	0	
J05070	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	24	4	6	0	
U43774	Fc fragment of IgA, receptor for	24	3	10	0	
AF052111	Homo sapiens clone 23953 mRNA sequence	19	7	2	0	
AA187563	ESTs, Highly similar to CGF-56 protein [H.sapiens]	23	3	7	0	
H12458	yj12d03.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148517 3' similar to WNT6	18	8	41	16	
Z23115	BCL2-like 1	25	1	21	1	Activated T Cells
U12471	Human thrombospondin-1 gene, partial cds	23	3	17	1	
L06895	MAX dimerization protein	18	8	6	0	
AB023211	peptidyl arginine deiminase, type II	18	8	8	0	
D63940	MAX-interacting protein 1	24	1	10	0	
X74039	plasminogen activator, urokinase receptor	21	3	7	0	
AB018293	KIAA0750 gene product	23	1	17	0	
AA978353	solute carrier family 1 (glutamate/neutral amino acid	21	2	3	0	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
	transporter), member 4					
AJ243797	three prime repair exonuclease 1	13	10	14	1	Activated T Cells
U89606	pyridoxal (pyridoxine, vitamin B6) kinase	20	3	8	0	
M19267	tropomyosin 1 (alpha)	20	2	8	0	
L35240	enigma (LIM domain protein)	17	4	12	0	
AL096737	Homo sapiens mRNA; cDNA DKFZp434F152 (from clone DKFZp434F152)	11	8	44	20	
D14689	nucleoporin 214kD (CAIN)	15	4	37	9	
U36341	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	19	0	26	2	Renal failure
M77016	tropomodulin	19	0	11	0	
U91316	cytosolic acyl coenzyme A thioester hydrolase	17	1	12	0	
M62896	Human lipocortin (LIP) 2 pseudogene mRNA, complete cds-like region	15	2	4	0	
L40904	peroxisome proliferative activated receptor, gamma	15	1	20	0	
U66359	T54 protein	15	0	13	0	
W28931	ESTs, Weakly similar to 38kDa splicing factor [H.sapiens]	12	3	27	2	
AB006537	interleukin 1 receptor accessory protein	11	2	1	0	
U97067	Cluster Incl U97067: Homo	12	1	6	0	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
	sapiens alpha-catenin-like protein mRNA, complete cds.					
U19599	BCL2-associated X protein	4	9	1	5	
AA628946	KH-type splicing regulatory protein (FUSE-binding protein 2)	9	3	39	5	
AI961220	serine protease inhibitor, Kazal type 1	12	0	4	0	
AL049250	Homo sapiens mRNA; cDNA DKFZp564D113 (from clone DKFZp564D113)	11	1	5	0	
AL031230	aldehyde dehydrogenase 5 family, member A1 (succinate- semialdehyde dehydrogenase)	11	0	3	0	
U68111	protein phosphatase 1, regulatory (inhibitor) subunit 2	10	1	18	1	
AF035819	macrophage receptor with collagenous structure	10	0	5	0	
AJ000480	phosphoprotein regulated by mitogenic pathways	9	1	5	0	
U58917	interleukin 17 receptor	8	2	1	0	
X90857	Conserved gene telomeric to alpha globin cluster	10	0	13	0	
J05500	spectrin, beta, erythrocytic (includes sperocytosis, clinical type I)	9	0	17	0	
X54412	collagen, type IX, alpha 1	8	1	24	4	
X75593	RAB13, member RAS	8	0	13	0	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
	oncogene family					
D38037	FK506-binding protein 1B (12.6 kD)	7	1	2	0	
J02854	myosin regulatory light chain 2, smooth muscle isoform	8	0	7	0	
AF034209	RIG-like 5-6	7	1	4	0	
U24578	complement component 4A	8	0	14	1	
AB011161	phosphatidylinositol-4- phosphate 5-kinase, type I, gamma	5	2	24	0	Renal failure
L23959	transcription factor Dp-1	6	1	2	0	
M64788	RAP1, GTPase activating protein 1	7	0	10	0	
X51362	dopamine receptor D2	6	0	20	1	
AB000520	adaptor protein with pleckstrin homology and src homology 2 domains	6	0	3	0	
U43843	Neuro-d4 (rat) homolog	6	0	5	0	
D43642	transcription factor-like 1	5	0	34	1	
W26700	ESTs, Highly similar to brain specific Na+-dependent inorganic phosphate cotransporter [R.norvegicus]	5	0	5	0	
AA844998	pancreatic polypeptide	5	0	11	0	
AJ223948	RNA helicase family	5	0	3	0	
AJ000644	speckle-type POZ protein	4	1	4	0	
W27095	B7 protein	3	2	13	16	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
AF032108	integrin, alpha 7	4	0	1	0	
M13207	colony stimulating factor 2 (granulocyte-macrophage)	4	0	7	0	
AF059202	diacylglycerol O-acyltransferase (mouse) homolog	3	1	10	0	
X82460	hydroxyprostaglandin dehydrogenase 15-(NAD)	3	1	3	0	
AJ011712	troponin T1, skeletal, slow	4	0	2	0	
L37127	polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	4	0	5	0	
AF089814	tumor suppressor deleted in oral cancer-related 1	3	1	2	0	
L07592	peroxisome proliferative activated receptor, delta	2	1	18	0	
AB020644	long fatty acyl-CoA synthetase 2 gene	2	1	4	0	
AF068706	adaptor-related protein complex 1, gamma 2 subunit	3	0	12	0	
AF059198	ER to nucleus signalling 1	2	1	16	1	
AF055027	coactivator-associated arginine methyltransferase-1	3	0	6	0	
L03785	myosin, light polypeptide 5, regulatory	1	2	8	0	
X91348	putative non-coding transcript (DiGeorge critical region 5)	2	0	1	0	
L32831	G protein-coupled receptor 3	1	1	16	2	
AI732885	Human BRCA2 region, mRNA sequence CG011	2	0	2	0	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
U96919	inositol polyphosphate-4-phosphatase, type I, 107kD	2	0	7	0	
U62433	cholinergic receptor, nicotinic, alpha polypeptide 4	2	0	8	1	
AF055000	H.sapiens mRNA for unknown liver orphan	1	0	43	15	
J05581	mucin 1, transmembrane	1	0	10	0	
U48213	D site of albumin promoter (albumin D-box) binding protein	1	0	14	18	
D45421	phosphodiesterase I/nucleotide pyrophosphatase 2 (autotaxin)	0	1	4	0	
AF017786	Phosphatidic acid phosphatase type 2b	1	0	3	0	
AB010419	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	1	0	11	0	
AF070587	Homo sapiens clone 24741 mRNA sequence	1	0	13	0	
AJ001481	double homeobox, 1	1	0	7	0	
U70732	glutamic-pyruvate transaminase (alanine aminotransferase)	1	0	22	2	
AF038171	Cluster Incl AF038171: Homo sapiens clone 23671 mRNA sequence.	1	0	3	0	
AF070629	RAB2, member RAS oncogene family	0	1	3	0	
L17330	pre-T/NK cell associated protein	1	0	3	0	

GenBank Accession Number	Gene Annotation	# Present RCC	# Present Normal	# Freq> 10 RCC	# Freq> 10 Normal	Common with
AI077476	KIAA0353 protein	1	0	7	0	
AF054185	proteasome (prosome, macropain) subunit, alpha type, 7	1	0	13	2	
U18548	G protein-coupled receptor 12	1	0	2	0	

Example 5. Probing the Molecular Basis of the RCC Disease Gene Classification Set in PBMCs

[0595] The expression profiles in RCC PBMCs were compared with profiles in RCC primary tumors. In these experiments the difference averages (rather than standard-curve normalized frequencies) of the 20 normal PBMCs and 45 RCC PBMCs from the present study were normalized using the GeneLogic GLGC normalization algorithm with difference averages detected in expression profiles of 57 normal kidney biopsies and 43 RCC tumor tissue biopsies. The expression profiles of normal kidney and primary RCC tumor tissues were downloaded *in silico* from the BioExpress database (Genelogic, Gaithersburg MD). To identify any genes induced in both RCC PBMCs and RCC tumor tissue relative to normal controls, gene expression values for the 165 arrays were clustered according to the method of Eisen *et al.*, Proc. Nat. Acad. Sci., U.S.A., 95: 14863-14868 (1998). In these analyses only genes were clustered and the original order of the arrays as depicted was conserved in order to visually detect batteries of genes with patterns of regulation consistent with RCC tumor markers present in RCC peripheral blood.

[0596] Expression profiles in RCC PBMCs were also compared with profiles in PHA-stimulated PBMCs *ex vivo*. In these experiments the expression profiles of 20 normal PBMCs and 45 RCC PBMCs were compared to expression profiles detected in (n=3) untreated or 6h PHA-stimulated PBMCs cultured *ex vivo*. Normalization using a standard curve to generate frequencies was performed, and hierarchical clustering of genes was subsequently performed.

[0597] In addition, the expression profiles in RCC PBMCs were compared with profiles in PBMCs from non-RCC patients with renal failure. The difference averages of the 20 normal PBMCs and 45 RCC PBMCs were normalized using the GeneLogic GLGC normalization algorithm with difference averages detected in expression profiles of 8 non-RCC renal failure PBMCs downloaded *in silico* from the BioExpress database (Genelogic, Gaithersburg MD). Hierarchical clustering of genes only was subsequently performed.

[0598] Furthermore, the 184 RCC disease genes listed in Tables 6 and 7 were compared to the 10 transcripts most strongly up-regulated in RCC tumors (n = 47) relative to normal kidney tissue (n = 60) using profiles downloaded from the Bioexpress Database (GeneLogic, Gaithersburg MD). The RCC tumor-specific transcripts that possessed the highest average fold differences in expression between RCC tumor tissue and normal kidney

were unchanged between normal and RCC PBMCs, suggesting that shed RCC tumor cells did not contribute significantly to the disease-associated transcripts identified in PBMCs isolated from RCC patients.

[0599] The 184 RCC disease genes listed in Tables 6 and 7 were also compared to genes differentially expressed between unstimulated CD4⁺ T cells (n = 3 normal donors) and CD4⁺ T cells (n = 3 normal donors) stimulated *ex vivo* with anti-CD3 and anti-CD28 in culture. Stimulated CD4⁺ T cells possessed 14 transcripts that were greater than 2-fold changed in the same direction (induced or repressed) as the disease-associated transcripts in RCC PBMCs, as indicated in the last column of Table 7.

[0600] The 184 RCC disease genes listed in Tables 6 and 7 were further compared to genes differentially expressed between PBMCs from non-RCC end-stage renal failure patients (n=9 individuals) and PBMCs from normal volunteers (n = 4 individuals). Of these, 9 transcripts differentially expressed in PBMCs from renal failure patients were also disease-associated transcripts in RCC PBMCs, as indicated in the last column of Table 7. Thus, the 184 RCC disease genes listed in Tables 6 and 7 contain a subset of markers commonly involved in immune responses measured *ex vivo* (CD4⁺ T cell activation) and in responses of circulating leukocytes to renal dysfunction observed *in vivo*. Without limiting the present invention to any particular theory, these results support a hypothesis that the expression levels of at least a subset of the disease-associated genes observed in RCC PBMCs may result from an activation of circulating T cells and/or other leukocytes in response to the presence of the tumor. In addition, it is possible that the regulation of another subset of disease-associated transcripts detected in RCC PBMCs may be due to alterations in leukocyte expression profiles in response to renal dysfunction in the RCC patients.

Example 6. Classification of RCC and RCC-Free Status Using Gene Expression Profiles in Peripheral Blood Cells

[0601] To build and train the RCC disease classifiers, 70% of the RCC PBMC expression patterns (n = 31) and 70% of the disease-free PBMC expression patterns (n = 14) were randomly selected and used as the training set. The remaining RCC and disease-free PBMC expression patterns were used as the test set. A relative class separation metric was used to calculate a measure of correlation and rank order the genes with expression levels most highly correlated with the classification vector characteristic of the training set. This measure of correlation is composed of mean expression values and variances.

[0602] Classification of the test set of samples was performed using a weighted voting method to classify the remaining PBMC expression profiles as characteristic of RCC or disease-free PBMCs. In this method the expression level of each gene in the classifier set contributes to an overall prediction strength which determines the classification of the sample. The prediction strength in this example is essentially a combined variable that indicates the number of "votes" for either one class or another, and can vary between 0 (narrow margin of victory) and 1 (wide margin of victory) in favor of the predicted class. To quantitate the accuracy of this prediction method, a value of 0.3 was imposed as the prediction strength threshold above which calls could confidently be made.

[0603] In this example, the accuracy of prediction for any given classifier gene set is defined as the percentage of calls with prediction strengths greater than 0.3 that also classifies samples correctly. The class predictors used in this example include (1) a 2-gene class predictor consisting of TLR2 and EEF1A2, (2) a 4-gene class predictor consisting of TLR2, LGALS3, EEF1A2, and BRF2, (3) a 6-gene class predictor consists of TLR2, LGALS3, DKFZP586E1621, EEF1A2, BRF2, and SNRPG, (4) an 8-gene class predictor consists of TLR2, LGALS3, DKFZP586E1621, SOD2, EEF1A2, BRF2, SNRPG, and NUMA1, (5) a 10-gene class predictor consists of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, EEF1A2, BRF2, SNRPG, NUMA1, and AKR1B1, (6) a 12-gene class predictor consists of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, and SMARCE1, (7) a 14-gene class predictor consists of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, and MSF, (8) a 16-gene class predictor consists of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, KIAA0410, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, MSF, and PTMA, (9) an 18-gene class predictor consists of TLR2, LGALS3, DKFZP586E1621, SOD2, DUSP6, KIAA0669, IL1RN, KIAA0410, T54, EEF1A2, BRF2, SNRPG, NUMA1, AKR1B1, SMARCE1, MSF, PTMA, and PSMD3, and (10) a 20-gene class predictor consists of EEF1A2, TLR2, BRF2, LGALS3, SNRPG, DKFZP586E1621, NUMA1, SOD2, AKR1B1, DUSP6, SMARCE1, KIAA0669, MSF, IL1RN, PTMA, KIAA0410, PSMD3, T54, C1QBP, and OSR1.

[0604] The accuracy of prediction for both the training sets and the test sets of RCC PBMCs with each set of predictor genes was calculated. Calculating the accuracy of classification for a training set indicates how uniformly the predictor gene set was positively correlated with each individual sample in the training set, whereas calculating the accuracy of prediction for a test set indicates how well the expression of this gene set predicted the

identity of individual samples in an “unknown” group. Table 8 illustrated the accuracy of prediction with each of the above-described class predictors. Classifier gene sets using 10 or more genes in the weighted voting algorithm yielded 100% accuracy in prediction of the test set. These studies demonstrate the feasibility of performing simple pair-wise prediction of RCC versus RCC-free status using expression patterns found in a limited number of gene transcripts in the compartment of peripheral blood.

**Table 8. Prediction Accuracy of the Class Predictors
of the Present Invention**

Genes in the Class Predictor	Prediction Accuracy for Training Set (%)	Prediction Accuracy for Test Set (%)
2	71.88	100.00
4	75.00	92.31
6	82.76	90.91
8	88.89	84.62
10	92.59	100.00
12	92.59	100.00
14	93.10	100.00
16	92.86	100.00
18	93.10	100.00
20	92.86	100.00

[0605] FIG. 3 shows a summary of the training set cross validation results for predictor gene sets of increasing size. A subset of RCC and normal PBMC samples (70%) were used as a “training set” to generate classifier gene sets, and then each predictor set was evaluated by cross validation to identify the predictor set with high accuracy for classification of the samples in the training set. Genecluster’s default correlation metric (Golub *et al.*, *supra*) was used to identify genes with expression levels most highly correlated with the classification vector characteristic of the training set. All of 5,249 genes meeting the initial filter criteria were screened using this approach.

[0606] Prediction was also performed in Genecluster using the weighted voting method. In this method, the expression level of each gene in the classifier set contributes to an overall vote on the classification of the sample (Slonim *et al.*, *supra*). The prediction strength is a combined variable that indicates the support for one class or the other, and can vary between 0 (narrow margin of victory) and 1 (wide margin of victory) in favor of the predicted class. Predictor sets containing between 2 and 20 genes were evaluated by leave

one out cross validation to identify the predictor set with the highest accuracy for classification of the samples in the training set (FIG. 3).

[0607] The 8 gene predictor set (89% accuracy) was selected for test set prediction. The 8 gene set consists of TLR2, LGALS3, DKFZP586E1621, SOD2, EEF1A2, BRF2, SNRPG, and NUMA1. FIG. 4 shows the relative expression levels of the 8 predictive genes in the training set. Each gene is represented by its respective qualifier. Graphically presented are the 4 genes elevated in RCC relative to normal PBMCs (TLR2, LGALS3, DKFZP586E1621, and SOD-2) and the 4 repressed genes in RCC relative to normal PBMCs (EEF1A2, BRF2, SNRPG, and NUMA1). The expression level increases, roughly, from dark to light and then to gray (or more precisely, the expression level increases from blue to red, as shown in FIG. 4 of the corresponding U.S. utility patent application filed November 21, 2003 and entitled "Methods for Diagnosing RCC and Other Solid Tumors").

[0608] The individual prediction confidence scores for each sample in the training set using this 8 gene classifier set are presented in FIG. 5A. For illustrative purposes, a positive sign was assigned to the prediction strengths resulting in votes for RCC and a negative sign was assigned to prediction strengths resulting in votes for normal PBMCs. A leave-one out cross validation was performed and the prediction strengths were calculated for each sample in the training set. Training set samples were ordered in the same order as in FIG. 4.

[0609] FIG. 5B illustrates the prediction results for the remaining test set of RCC and normal PBMC samples using the 8 gene predictor set. On the test set, the predicted class matched the true class in all cases, though for one of the 19 test samples the prediction strength was negligible. These studies demonstrate the feasibility of predicting RCC versus disease-free status using expression patterns found in a limited number of gene transcripts in mononuclear cells from peripheral blood.

Example 7. Differentially Expressed Genes in RCC Tumor Tissues and Non-RCC End-Stage Renal Failure Patients

[0610] Expression profiles of RCC PBMCs were compared with expression profiles of RCC tumor tissue or PBMCs from patients with renal failure. In each comparison, a multivariate (hierarchical clustering) analysis was employed to search for co-regulated batteries of genes between the groups, followed by a fold-change analysis and Student's *t*-test to support any findings. In the first analysis, expression profiles of RCC PBMCs were compared *in silico* with expression profiles of RCC tumor tissues (n = 43 biopsies) from the

GeneLogic BioExpress database (Gaithersburg, MD). All samples were ordered in a supervised fashion (*i.e.*, no arrays were clustered) and genes were ordered using a hierarchical clustering approach to identify gene sets upregulated in both PBMCs of RCC patients and RCC tumor biopsies compare to disease-free controls. Fold change analysis identified 24 RNA species that were statistically significant ($p < 0.05$, Student's *t*-test) and greater than 2-fold induced in RCC PBMCs relative to disease-free PBMCs and in RCC tumors relative to disease-free kidney tissue.

[0611] These 24 RNA species correspond to FABP5, SCYA20, ADM, COPEB, FCGR3B, UNK_M62896, FN1, HMOX1, ITGA7, DGCR5, CBP2, UNK_AL049250, SLC1A4, MMP9, SLC16A3, LILRB3, FCGR1A, LHFPL2, PLEC1, S100A11, SPOP, CCR1, TLR2 and KIAA0750, respectively. In addition, these 24 RNA species are capable of hybridizing under stringent conditions to CPSs 57, 229, 92, 91, 221, 26, 236, 207, 16, 8, 245, 152, 2, 58, 192, 19, 99, 28, 191, 138, 143, 61, 1, and 148, respectively.

[0612] In the second analysis, PBMCs from non-RCC end-stage renal failure patients ($n=8$ individuals) were compared with PBMCs from disease-free volunteers and patients with RCC. Hierarchical clustering of genes in these groups of samples identified several clusters of genes that appear to be similarly regulated between advanced RCC patients and patients with end-stage renal failure. Fold change analysis identified a plurality of RNA transcripts that were statistically significant ($p < 0.05$, Student's *t*-test) and greater than 2-fold induced in RCC PBMCs and in PBMCs from non-RCC patients with renal failure relative to disease-free PBMCs. The CPSs capable of hybridizing to these RNA transcripts under stringent conditions are depicted in Table 9. The genes corresponding to the CPSs are also indicated.

Table 9. RCC Disease Genes that Are Differentially Expressed in Non-RCC Renal Failure Patient Relative to Disease-free PBMCs

CPS No.	Corresponding Genes
92	ADM
91	COPEB
34	AQP9
222	PTGS2
244	STIP1
53	SOD2
151	PDXK

CPS No.	Corresponding Genes
18	IL1RN
21	ANXA5
109	IFIT4
211	IL1B
201	GRO1
104	PLAUR
130	NP
58	MMP9
192	SLC16A3
19	LILRB3
99	FCGR1A
28	LHFPL2
191	PLEC1
138	S100A11
143	SPOP
61	CCR1
1	TLR2
148	KIAA0750
105	CDC34
158	POLR2J
10	ETS2
125	MAD
52	GPR3
11	PIP5K1C
220	PRF1
178	PSMA7
154	INPP4A
12	TCFL1
47	DGAT
146	S100P
165	DOC-1R
62	C8FW
128	PDI2
133	GEF-2
147	TNNT1
111	BSG
84	IL17R
227	HK3
115	RALBP1
195	RNASE2

CPS No.	Corresponding Genes
25	TPM1
40	BLVRB
35	APS
17	PPARD
157	NFE2
14	IL1RAP
173	S100A12
174	CD9
9	ENIGMA
135	HAGH
247	NCF1
250	FLOT1
94	ITGA2B
148	KIAA0750
194	FKBP8
4	DUSP6
87	CBFA2T3

[0613] The genes and CPSs listed in Table 9 can be used as markers for renal failure and other types of renal dysfunction.

Example 8. Prediction of RCC Status Versus Disease-free Volunteers and Patients with Other Solid Tumors

[0614] In this analysis, expression profiles were compared simultaneously among four classes of PBMCs which include RCC PBMCs, disease-free PBMCs, prostate cancer PBMCs, and head and neck cancer PBMCs. An initial hierarchical analysis demonstrated the global transcriptional relationships between the expanded database of PBMC expression profiles. 70% of the samples were then used as a training set, and a multi-class correlation metric was employed to identify and rank the genes most highly correlated with each class of PBMC expression profile (RCC, disease-free, prostate carcinoma, head and neck) in the database. A 20-gene classifier was determined. These genes and the corresponding CPSs are illustrated in Table 10. This 20-gene set can be used to predict each class versus all other classes.

[0615] The ability of this gene set to predict the remaining 30% of the samples as RCC versus non-RCC was calculated. The gene set was able to predict each remaining PBMC profile in the test set as RCC or non-RCC with 89% or 92% accuracy, respectively.

As appreciated by one of ordinary skill in the art, a subset of these 20 genes, such as 2, 4, 6, 8, 10, 12, 14, 16 or 18 genes, can be used to predict RCC from non-RCC. Non-RCC includes other solid tumors, such as prostate cancer or head/neck cancer.

Table 10. Gene Set For Predicting RCC Versus Disease-free Volunteers and Patients with Other Solid Tumors

CPS No.	Corresponding Genes
268	CD44
269	CRADD
270	CCRL2
71	KIAA0837
271	KIAA0707
272	KIAA1113
64	EREG
273	UNK AL050119
17	PPARD
37	CTSL
59	ATP2B1
274	UNK AF052115
275	MITF
276	STAT3
264	KIAA0410
277	TPD52L2
278	UNK AI732885
31	MARCO
69	LOC64116 (also referred to as UNK AL049963)
50	PDNP2

Example 9. Identification of A Solid Tumor-Free Predictor Gene Set

[0616] Supervised analysis of expression profiles in disease-free PBMCs and PBMCs from different solid tumors was conducted. PBMC expression profiles from 3 out of 5 Head/Neck cancer patients, 14 out of 20 disease-free volunteers, 11 out of 15 prostate cancer patients, and 32 out of 45 RCC patients were classified, and a k-nearest neighbor's algorithm calculated the genes most highly correlated with each class distinction. The 19 top genes with expression patterns most highly correlated with these PBMCs from head/neck patients, disease-free volunteers, prostate cancer patients, and RCC patients were identified. The top 19 genes thus identified were then used to determine the accuracy of prediction of solid-tumor versus solid tumor-free status in the remaining PBMC samples. A weighted voting

method was used to determine the prediction strength for each sample. These 19 genes are listed in Table 11.

Table 11. A Solid Tumor-Free Predictor Gene Set

CPS No.	Corresponding Genes	Entrez Accession No.
258	NUMA1	Z11584
285	CXCR4	L06797
107	IL10RA	U00672
286	M9	AB019392
287	FAU	X65923
256	BRF2	U07802
288	RPS6	X67309
255	EEF1A2	X70940
289	BAG5	AB020680
259	AKR1B1	X15414
290	UNK AL022721	AL022721
266	C1QBP	M69039
291	DKZP586E0820	AL050147
292	NONO	U02493
265	PSMD3	D67025
131	UNK N74607	N74607
293	UNK AI743507	AI743507
294	MAPKAPK5	AF032437
295	UNK U79297	U79297

[0617] The foregoing description of the present invention provides illustration and description, but is not intended to be exhaustive or to limit the invention to the precise one disclosed. Modifications and variations are possible consistent with the above teachings or may be acquired from practice of the invention. Thus, it is noted that the scope of the invention is defined by the claims and their equivalents.

What is claimed is:

1. A method, comprising the steps of:
 - providing at least one peripheral blood sample of a human; and
 - comparing an expression profile of one or more genes in said at least one peripheral blood sample to at least one reference expression profile of said one or more genes, wherein each of said one or more genes is differentially expressed in peripheral blood mononuclear cells (PBMCs) of patients having a solid tumor as compared to PBMCs of disease-free humans, provided that if said one or more genes consist of only one gene, said one gene is not selected from the group consisting of IL1B, IL6, MMP-9 and FCGR3B, and further provided that if said one or more genes consist of two genes, said two genes are not IL1B and IL6.
2. The method according to claim 1, wherein said solid tumor is selected from the group consisting of RCC, prostate cancer, and head/neck cancer.
3. The method according to claim 2, wherein said peripheral blood sample comprises enriched PBMCs.
4. The method according to claim 2, wherein, said peripheral blood sample is a whole blood sample.
5. The method according to claim 2, wherein the expression profile is determined using quantitative RT-PCR or an immunoassay.
6. The method according to claim 1, wherein said at least one reference expression profile comprises an expression profile of said one or more genes in peripheral blood samples of disease-free humans.
7. The method according to claim 6, wherein said at least one reference expression profile further comprises an expression profile of said one or more genes in peripheral blood samples of patients having said solid tumor.

8. The method according to claim 7, wherein said one or more genes include at least two genes, and the expression profile of the human is compared to said at least one reference expression profile using a weighted voting algorithm.

9. The method according to claim 6, wherein each of said one or more genes is differentially expressed in PBMCs of patients having another solid tumor relative to disease-free humans.

10. The method according to claim 9, wherein said solid tumor and said another solid tumor are different tumors selected from the group consisting of RCC, prostate cancer, and head/neck cancer.

11. The method according to claim 1, wherein said one or more genes include at least one gene selected from Table 4 or Table 6.

12. The method according to claim 1, wherein said one or more genes include at least one gene which has an RNA transcript capable of hybridizing under stringent conditions to a classification probe sequence (CPS) selected from Table 2.

13. The method according to claim 1, wherein said one or more genes include at least one gene which has an RNA transcript capable of hybridizing under stringent conditions to a qualifier selected from Attachment A.

14. The method according to claim 1, wherein said one or more genes include at least two genes selected from Table 4.

15. The method according to claim 1, wherein said one or more genes include a classifier identifiable using a two-class or multi-class correlation metric algorithm.

16. A method, comprising the steps of:
providing at least one peripheral blood sample of a human having a non-blood disease; and

comparing an expression profile of one or more genes in said at least one peripheral blood sample to at least one reference expression profile of said one or more

genes, wherein each of said one or more genes is differentially expressed in PBMCs of patients having the non-blood disease as compared to PBMCs of disease-free humans.

17. The method according to claim 16, wherein the non-blood disease is a solid tumor selected from the group consisting of RCC, prostate cancer, and head/neck cancer.

18. A method for identifying a gene which is differentially expressed in peripheral blood samples of non-blood disease patients as compared to peripheral blood samples of reference humans, comprising the steps of:

providing an expression profile of one or more genes in peripheral blood samples of said non-blood disease patients;

providing a reference expression profile of said one or more genes in peripheral blood samples of said reference humans; and

comparing the expression profile to the reference expression profile to identify a gene that is differentially expressed in said non-blood disease patients relative to said reference humans.

19. A kit comprising:

one or more polynucleotides, each of said one or more polynucleotides capable of hybridizing under stringent conditions to an RNA transcript, or the complement thereof, of a gene differentially expressed in PBMCs of patients having a solid tumor as compared to PBMCs of disease-free humans; or

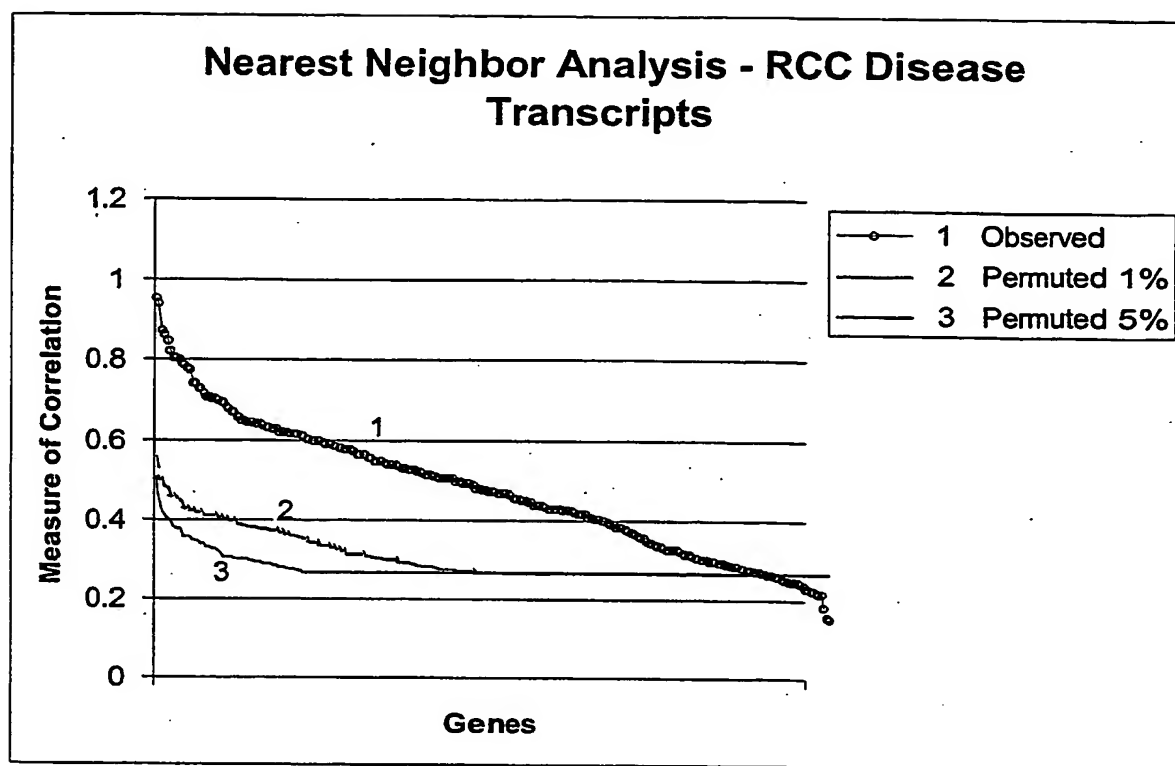
one or more antibodies, each of said one or more antibodies capable of binding to a polypeptide encoded by a gene differentially expressed in PBMCs of patients having a solid tumor as compared to PBMCs of disease-free humans.

20. A system comprising:

a memory which stores at least one reference expression profile of one or more genes in peripheral blood samples of reference humans, wherein each of said one or more genes is differentially expressed in PBMCs of patients having a non-blood disease as compared to PBMCs of disease-free humans;

a program capable of comparing an expression profile of interest to said at least one reference expression profile; and

a processor capable of executing the program.

**FIG. 1**

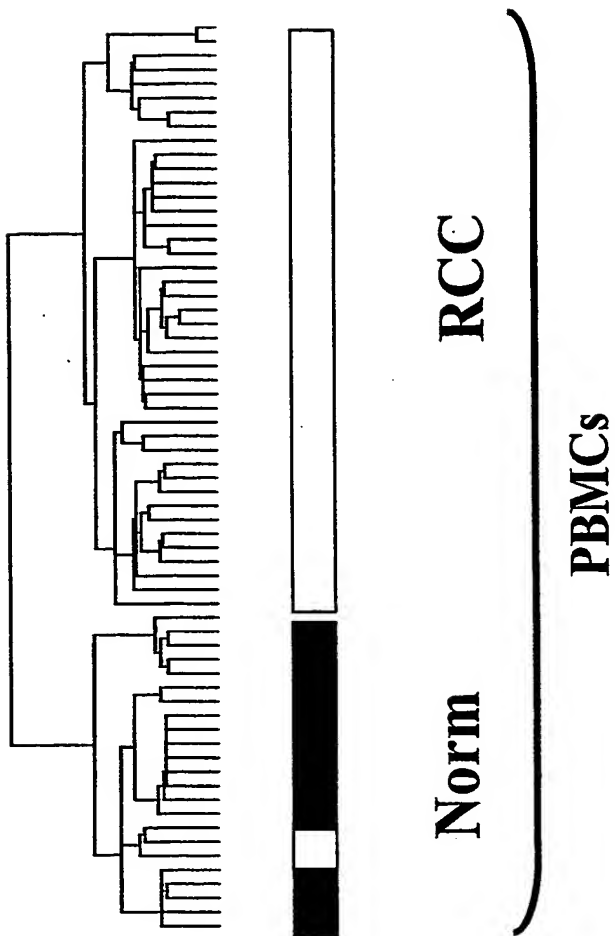
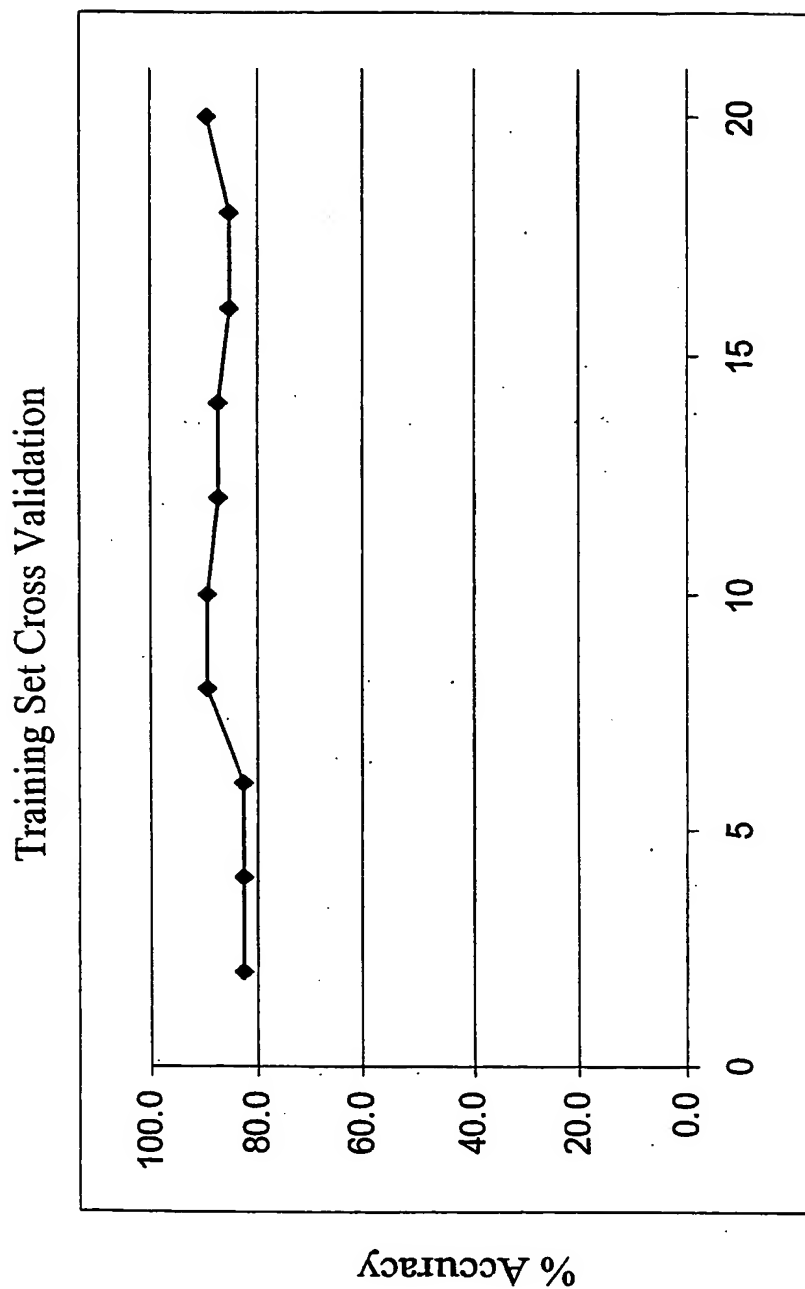


FIG. 2



Number of Genes in Predictor

FIG. 3

Disease-Free
Samples

RCC Samples

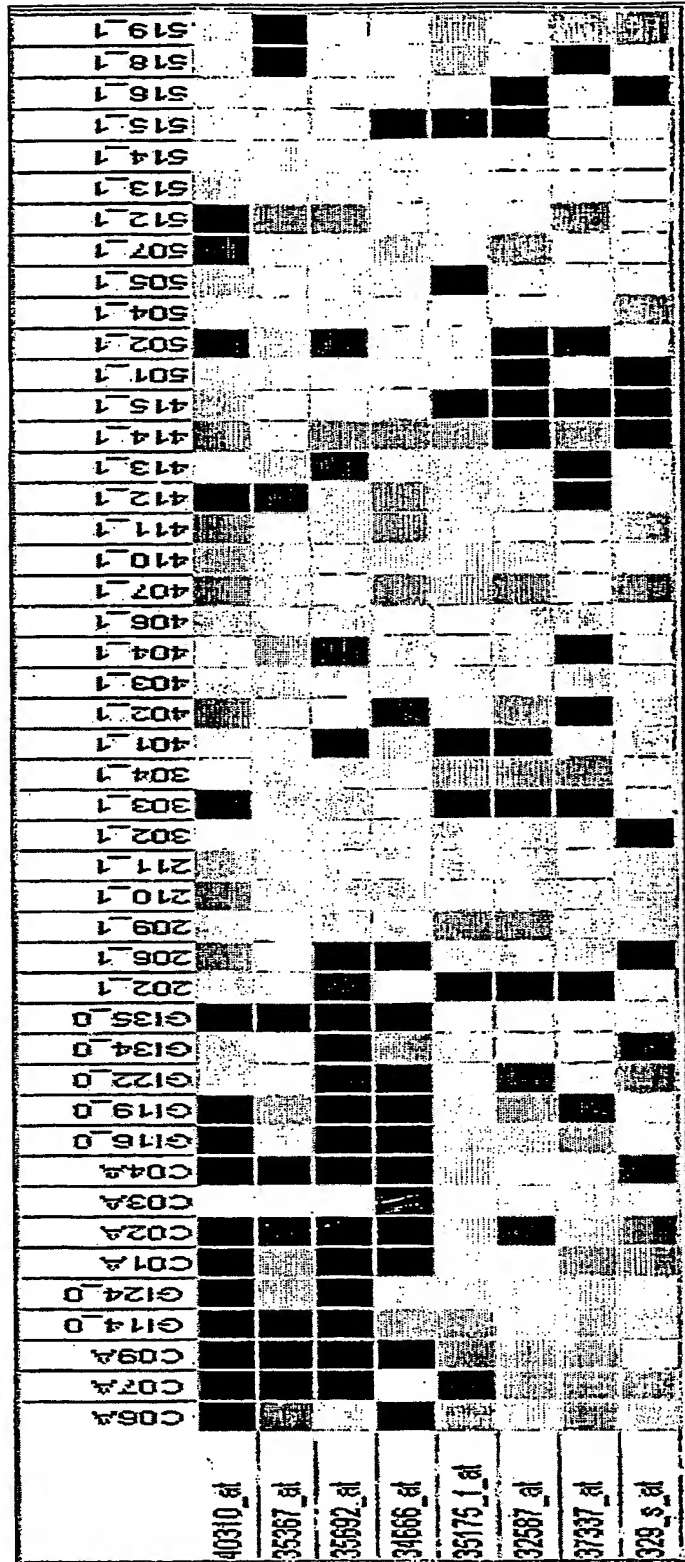


FIG. 4

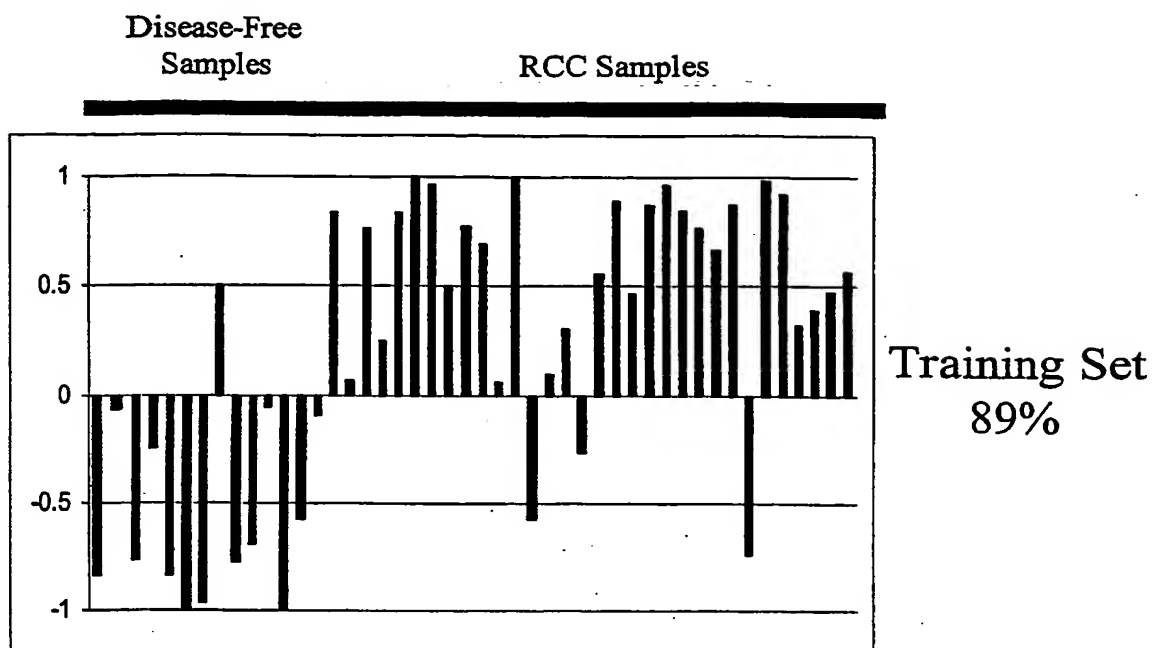


FIG. 5A

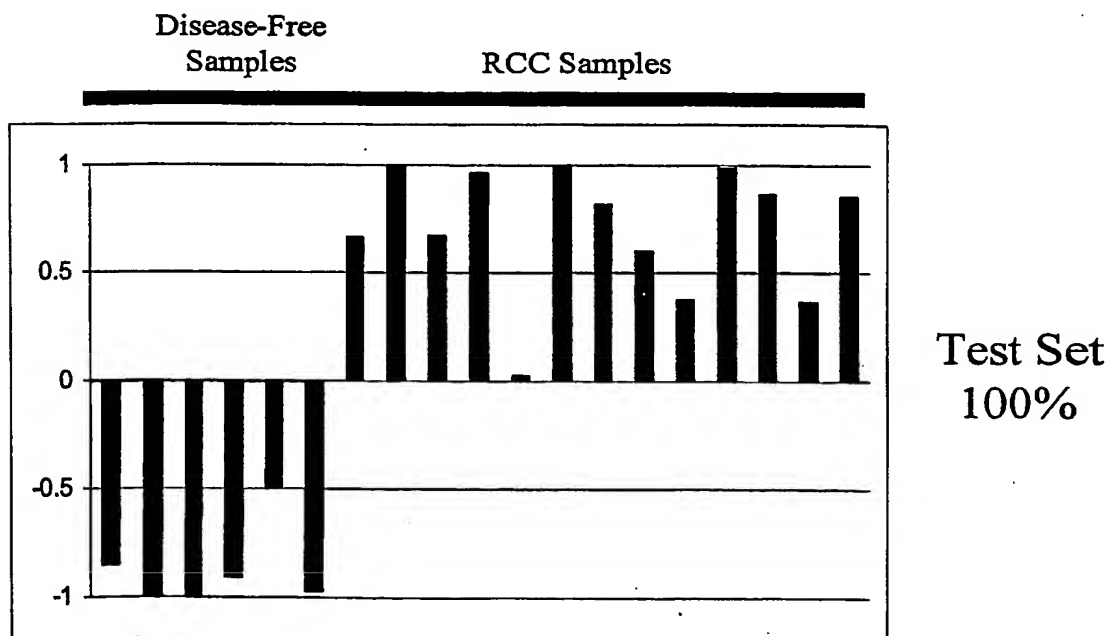


FIG. 5B

ATTACHMENT A. OLIGONUCLEOTIDE PROBES

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40310_at	332	TTTCCGTCCTTTTGATGAGAACAAT
40310_at	333	AAGACCTACCTGGAGTGGCCCATGG
40310_at	334	ACCTACCTGGAGTGGCCCATGGACG
40310_at	335	TAAATCTGAGAGCTGCGATAAAGTC
40310_at	336	GATAAAGTCCTAGGTTCCCATATTT
40310_at	337	AGGTTCCCATATTTAAGACCAGTCT
40310_at	338	CCAGTCCTTGTCTAGTTGGGATCTT
40310_at	339	TATAAAACTACGTGGATGTACCGT
40310_at	340	AACTACGTGGATGTACCGTCATTTG
40310_at	341	ACTACGTGGATGTACCGTCATTTGA
40310_at	342	GTGGATGTACCGTCATTTGAGGACT
40310_at	343	TCATTTGAGGACTTGCTTACTAAAA
40310_at	344	TGAGGACTTGCTTACTAAAACTACA
40310_at	345	TACAAAACTTCAAATTTTGTCTGGG
40310_at	346	CTTCAAATTTTGTCTGGGGTGCTGT
40310_at	347	ATGAGATAACCATGATCATAAGTCT
41126_at	348	GAAGCAAACCTGTTAATCTTCGAAAA
41126_at	349	TTTCACTTCTTGGATATCAAGTGCT
41126_at	350	GATATCAAGTGCTAACCCAGTATGT
41126_at	351	ACAGAGTCCTTTCTGCTGGTGAGGA
41126_at	352	TTTCTGCTGGTGAGGACAGCATTTT
41126_at	353	GAGCAGGGCTTTGTTCTCTATGTGC
41126_at	354	GCCCTTGTTCTGTGTGTAGTTACTT
41126_at	355	TGTAGTTACTTGACAGCATCAAATG
41126_at	356	TTGACAGCATCAAATGCCGCCTCTT
41126_at	357	TGACAGCATCAAATGCCGCCTCTTC
41126_at	358	TGTCCTTCAAGTTTTTCATGAAGTAG
41126_at	359	GTCCTTCAAGTTTTTCATGAAGTAGC
41126_at	360	GTTCTGGGCGCCTGATTTTGCTGTG
41126_at	361	TTCTGGGCGCCTGATTTTGCTGTGA
41126_at	362	GATTTTGCTGTGACTCCCAGACCCA
41126_at	363	ATCTGAGAGCGTGCTGTTTGTGGCT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35367_at	364	ACAATTCTGGGCACGGTGAAGCCCA
35367_at	365	ACGGTGAAGCCCAATGCAAACAGAA
35367_at	366	CCACGCTTCAATGAGAACAACAGGA
35367_at	367	CACGCTTCAATGAGAACAACAGGAG
35367_at	368	CGCTTCAATGAGAACAACAGGAGAG
35367_at	369	GACAGTCGGTTTTCCCATTTGAAAG
35367_at	370	GAAATCAGCAAACCTGGGAATTTCTG
35367_at	371	CAGCAAACCTGGGAATTTCTGGTGAC
35367_at	372	CAAACCTGGGAATTTCTGGTGACATA
35367_at	373	GGAATTTCTGGTGACATAGACCTCA
35367_at	374	GAATTTCTGGTGACATAGACCTCAC
35367_at	375	TGACATAGACCTCACCAGTGCTTCA
35367_at	376	GACATAGACCTCACCAGTGCTTCAT
35367_at	377	GAATCTAAACCTTACATGTGTAAAG
35367_at	378	ATCTAAACCTTACATGTGTAAAGGT
35367_at	379	ACCTTACATGTGTAAAGGTTTCATG
41193_at	380	GCAGTATGCCACTTCTTAAACAGA
41193_at	381	ATTGTGCTCTTTTCTAATCCAAAGG
41193_at	382	TAATCCAAAGGGTATATTTGCAGCA
41193_at	383	GGTATATTTGCAGCATGCTTGACTT
41193_at	384	GCTTGACTTTACCAATTCTGATGAC
41193_at	385	ACCAATTCTGATGACATCTTTACGG
41193_at	386	GATGACATCTTTACGGACACTATTA
41193_at	387	GGACACTATTATCACTAAGACCTTG
41193_at	388	CGAAGTCTTTAGTCTTTTTCATGTA
41193_at	389	TCTCTTTATGTAGTTTGACTATGCC
41193_at	390	GTAGTTTGACTATGCCTTACCTTTG
41193_at	391	AATTCCTCAGGGAGTGTCACCTCAA
41193_at	392	CTCAAATGCAATACTTTGGGTTGGT
41193_at	393	TGTGAGCATGGGTACCCATTTGATA
41193_at	394	GTACCCATTTGATAAGAGAAATGCA
41193_at	395	AGAGTTAAATTCTCCATTATGTTCTG
38829_r_at	396	TGCGGGTGCTGTCTGTCTCCCCCCC
38829_r_at	397	GGTGCTGTCTGTCTCCCCCCCCTTTC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38829_r_at	398	GTGCTGTCTGTCTCCCCCCTTTCC
38829_r_at	399	CTTCCCTCCCTGTAGTTTTGAAGCG
38829_r_at	400	CCCTCCCTGTAGTTTTGAAGCGGAT
38829_r_at	401	AGTTTTGAAGCGGATGTTTGTTCTT
38829_r_at	402	TTTTGAAGCGGATGTTTGTTCTTTA
38829_r_at	403	AAGCGGATGTTTGTTCTTTATAGAT
38829_r_at	404	CGGATGTTTGTTCTTTATAGATGTT
38829_r_at	405	TTCTTTATAGATGTTGTTTAAAAAG
38829_r_at	406	GTTTAAAAAGCCTGATAATGGTGAT
38829_r_at	407	TTTAAAAAGCCTGATAATGGTGATT
38829_r_at	408	AAAAAGCCTGATAATGGTGATTGAA
38829_r_at	409	AAGCCTGATAATGGTGATTGAAATT
38829_r_at	410	AGCCTGATAATGGTGATTGAAATTT
38829_r_at	411	CAATGTGCTTTCCTAACCGTGCCCC
41102_at	412	TGCGGTTTGTGGACAACATGTACAA
41102_at	413	ATTGAAGATGTCCTAAGCCCAGATA
41102_at	414	CCTAAGCCCAGATACCTGTGTATGT
41102_at	415	CCCAGATACCTGTGTATGTTCGGACA
41102_at	416	TGTCGGACAGATGAAGGCCGAGTCC
41102_at	417	ATGAAGGCCGAGTCCTGGAAGGCCT
41102_at	418	TCCTGGAAGGCCTGAGGGAAGACAT
41102_at	419	GAAGACATGCTGGAGACCCTGGTTC
41102_at	420	AAGACATGCTGGAGACCCTGGTTCC
41102_at	421	GACATGCTGGAGACCCTGGTTCCCA
41102_at	422	TTCCCAAGGCAGAGGGTGACCGTGT
41102_at	423	GAGCCGGGCTTTGGTGCAACTGCCA
41102_at	424	ACTGCCAAGAGAAAATCAGGTGGTG
41102_at	425	CATCCTCTACTTCTGGTGCAAGTCCT
41102_at	426	ATCCTCTACTTCTGGTGCAAGTCCTG
41102_at	427	TACTTCTGGTGCAAGTCCTGGGACAA
40210_at	428	CTGATTTATTCTGTTACTAGATCAG
40210_at	429	AGATCAGGTTTTAGGGTCCTGCAAA
40210_at	430	AGGGTCCTGCAAAAGGCTAGCTCGG
40210_at	431	CTGCAAAAGGCTAGCTCGGCACTAC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40210_at	432	AGCTCGGCACTACACTAGGGAATTT
40210_at	433	GGAATTTGCTCCTGTTCTGTCACTT
40210_at	434	TGAGGCTTTTAGTTCCCTGGCCCCG
40210_at	435	ACATCTTGCTCAAGTCAGGAGGCCG
40210_at	436	GCTCAAGTCAGGAGGCCGGAGATCA
40210_at	437	CAAGCCTCCCAGTACTGACCTGAAA
40210_at	438	TACTGACCTGAAAACCTTGTGACAAG
40210_at	439	CACCAACAAGTGCTCCCTGGGCTGA
40210_at	440	CTCCCTGGGCTGAGGACCCTTTCTT
40210_at	441	CCTGGGCTGAGGACCCTTTCTTGCC
40210_at	442	ACCCCGGAAGCTGAACCTGAGGGAG
40210_at	443	TGAACCTGAGGGAGACAACGGCAGA
37069_at	444	ACAGGCAGCCACCTGGACACAAACA
37069_at	445	AGACTCCACAGCAGAACTCCCAGGG
37069_at	446	GACTCCACAGCAGAACTCCCAGGGA
37069_at	447	GGCATGGCTTCAGAGCACCAGGCAG
37069_at	448	CTTGGCCTCGGGAAATGTAGCTGGA
37069_at	449	TGTAGCTGGAGTCATCATTTAGCAG
37069_at	450	TGGAGTCATCATTTAGCAGAGCACG
37069_at	451	CATCATTTAGCAGAGCACGGTGTCC
37069_at	452	TGGACAGAGGCCTCCGGTCAGCCTC
37069_at	453	CTCTCACTGGACAGCATCACCTGGA
37069_at	454	CACTGGACAGCATCACCTGGACACA
37069_at	455	ACAGCATCACCTGGACACAGAGCCT
37069_at	456	GGACACAGAGCCTCACCTAGTCTGT
37069_at	457	TTTGCTTTGGACAGTGACACCAAGA
37069_at	458	TTGGACAGTGACACCAAGAATACTC
37069_at	459	GACAGTGACACCAAGAATACTCACC
39530_at	460	TCATGCACGCCCTGAAGATGACCTG
39530_at	461	CCTGAAGATGACCTGGCACGTGCAC
39530_at	462	GATGACCTGGCACGTGCACTGCTTT
39530_at	463	CACTGCTTTACCTGTGCTGCCTGCA
39530_at	464	TGCAAGACGCCCATCCGGAACAGGG
39530_at	465	GCAAGACGCCCATCCGGAACAGGGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39530_at	466	CGGAACAGGGCCTTCTACATGGAGG
39530_at	467	GGAACAGGGCCTTCTACATGGAGGA
39530_at	468	GAACAGGGCCTTCTACATGGAGGAG
39530_at	469	AAGATGTTTGGCACGAAATGCCATG
39530_at	470	GTTTGGCACGAAATGCCATGGCTGT
39530_at	471	GCACGAAATGCCATGGCTGTGACTT
39530_at	472	CACGAAATGCCATGGCTGTGACTTC
39530_at	473	TGACTTCAAGATCGACGCTGGGGAC
39530_at	474	ACTTCAAGATCGACGCTGGGGACCG
39530_at	475	TCGACGCTGGGGACCGCTTCCTGGA
38739_at	476	CATTCATTCGGAGAAAACGTTTTGA
38739_at	477	TCGTTTCAAAAGAGCACCTGAGTCA
38739_at	478	CACCTGAGTCATGTGTATTCCCGGC
38739_at	479	TGACCCGGTCAAGTTGGTTTCAAAG
38739_at	480	CGACAGGCTTGTCTGTTTACTAGCT
38739_at	481	TCCTGTGATGAAACTGAGGAATCGG
38739_at	482	ATCCCAGTATACATAAGCACAGGA
38739_at	483	TTCTCAAGAGGGATGTATTTATCAC
38739_at	484	GTATTTATCACTTGGACATCTGTTT
38739_at	485	CTGCCAAAAGAATCCTAGGCAGTGG
38739_at	486	TCATTGTATGTGAGGTTGAACCACG
38739_at	487	GAAATTGCCAATATTAGGCTGGCTT
38739_at	488	CTGGCTTTTATCTACAAAGAAGGAG
38739_at	489	AGTTTCATGGGGTTCAGCCTAACAG
38739_at	490	ACCATTGGCATGGTAATAAACAGAT
38739_at	491	TGTAATTGGGCCTTTACTCTCTCAA
32133_at	492	TGTCCACTGAGAACGTGGGCAGTGT
32133_at	493	GAGAACGTGGGCAGTGTCCAAATTC
32133_at	494	TCCTGTACTGTAAAGACTAAAAGGC
32133_at	495	GACTAAAAGGCGTTTGCTCTGAGAC
32133_at	496	AGGCGTTTGCTCTGAGACTGACAAG
32133_at	497	CTTCACCATGGTACTGTCTCCACAG
32133_at	498	TGGTACTGTCTCCACAGCCCTCAGT
32133_at	499	AAATGAAACTGCAAACCTCGTGTGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
32133_at	500	GCAAACCTCGTGTGTCTTAACCTCCC
32133_at	501	CGCCCCGTGGTCTGGTGCGTGACAA
32133_at	502	TCCAAAGCGCCGAGACGAGGGTGCT
32133_at	503	CCGAGACGAGGGTGCTGTGTCCCTC
32133_at	504	TGTGTCCCTCAAACCCAGAGTGGTG
32133_at	505	GTGGGCGCCTCTGAAACCATAACAGC
32133_at	506	TCTGAAACCATAACAGCCACTCCTGG
32133_at	507	TTTAGAGATCTCTCTAATAAATCGG
33873_at	508	ATGCCACTGCTCGAGCCTTCAAGAT
33873_at	509	AGAAGTACATTACTGCCCATGGACT
33873_at	510	GAAGTACATTACTGCCCATGGACTG
33873_at	511	AAGAGATGTCTAGTCCTCAGAACT
33873_at	512	GATGTCTAGTCCTCAGAACTTCTT
33873_at	513	GAAACTTCTTTCCTGCCCTGATTGG
33873_at	514	CCTGATTGGGGCTCTTGCTGTTCCG
33873_at	515	TTGCTGTTCCGTTTCTTCTCCCTGC
33873_at	516	CCTAGTTCTTACAGGTTTCGTTGTG
33873_at	517	CTAGTTCTTACAGGTTTCGTTGTGT
33873_at	518	TTGTGCGCGATGGTGAGTCCTGTTA
33873_at	519	TTACAAGTCGAGGACGCCGCGAATT
33873_at	520	AGGACGCCGCGAATTTAGTAGAGGT
33873_at	521	GACCCTGTTACAGACATACCCTATG
33873_at	522	AGACATACCCTATGCCACTGCTCGA
33873_at	523	CTATGCCACTGCTCGAGCCTTCAAG
39854_r_at	524	ATGCGCAACAACCTCTCGCTGGGGG
39854_r_at	525	CCGAAGCTCTGCGCATGCGCGCACC
39854_r_at	526	CCCCGCGGACCCAGCATCCCCGCAG
39854_r_at	527	CCGCGGACCCAGCATCCCCGCAGCA
39854_r_at	528	CCTGCTCCCGAGGCCCGGCCCGTGA
39854_r_at	529	GGAACCCTGCCTGAGACGCCTCCAT
39854_r_at	530	GAGACGCCTCCATTACCACTGCGCA
39854_r_at	531	ACGCCTCCATTACCACTGCGCAGTG
39854_r_at	532	CCACTGCGCAGTGAGATGAGGGGAC
39854_r_at	533	AGGGGACTCACAGTTGCCAAGAGGG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39854_r_at	534	ACTCACAGTTGCCAAGAGGGGTCTT
39854_r_at	535	CCTCCCCTGGGCCGCTGAGGCCCCG
39854_r_at	536	GTGCTGCCCAGACCTCCCCCGCC
39854_r_at	537	GAACCTTGCAGCTGCCCTTCCCTCC
39854_r_at	538	TTTGCAGCTGCCCTTCCCTCCCCGT
39854_r_at	539	AGAATTATTTATTTTCGCCAAAGCA
38546_at	540	CTGCATTCCTTTTGCACCTTTTGGAT
38546_at	541	GCATTCCTTTTGCACCTTTTGGATTC
38546_at	542	TATATGCCTGCCTTTGGTACTTAAT
38546_at	543	ATGCCTGCCTTTGGTACTTAATTTT
38546_at	544	AATATATGCTATAGGGACGTTCCAT
38546_at	545	GCTATAGGGACGTTCCATGCCCAGG
38546_at	546	TATAGGGACGTTCCATGCCCAGGTT
38546_at	547	CGTTCCATGCCCAGGTTAACAAAGA
38546_at	548	TTCCATGCCCAGGTTAACAAAGAAC
38546_at	549	CCATGCCCAGGTTAACAAAGAACTG
38546_at	550	CATGCCCAGGTTAACAAAGAACTGT
38546_at	551	ATGCCCAGGTTAACAAAGAACTGTG
38546_at	552	TCTCTTCTGTATTGTAACCTTAGATG
38546_at	553	CTCTTCTGTATTGTAACCTTAGATGA
38546_at	554	TAACTTAGATGATTCCCAAGGACTC
38546_at	555	AGATGATTCCCAAGGACTCTAATAA
1856_at	556	ATGCTTCTAATGCTTGCATTTACAA
1856_at	557	ACAATGCCGATGACATAGTCGGAAT
1856_at	558	TGGAAGCGTCATCCATGCCATCAGC
1856_at	559	TATATGGTATTTCTGATCCCAACAT
1856_at	560	CTGATCCCAACATGCTGTCTAATTG
1856_at	561	CTAATTGTTCTGTGAATATGATGAC
1856_at	562	CAACCAGCAGTGACAGCATGGGAGA
1856_at	563	ATAATCCAAGACTTCTGAGCATGAA
1856_at	564	ACTTGAGACAGCTCCATCAGATGTC
1856_at	565	GACAGCTCCATCAGATGTCCTCTTC
1856_at	566	TCCATCAGATGTCCTCTTCCAGTAT
1856_at	567	CCAGTATGTCAGCAGGCGCCAATTC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1856_at	568	TTTACAATCAGATGCATTTGAGGG
1856_at	569	TTGAGGGATCTGACTTCAGTTGTGC
1856_at	570	ACTTCAGTTGTGCAGATAACAGCAT
1856_at	571	AGTATTCAGGTATTGGCAGTATGCA
36892_at	572	CCTGAGGAACAACCTGGGGCAGCCCC
36892_at	573	CTTCCCCAGAGATGGCTCCTTGGGA
36892_at	574	CCAGAGATGGCTCCTTGGGATGAAG
36892_at	575	AGGATCGGCTTCCTCAGGGGCACAG
36892_at	576	AACTTCCCCTTAGAGTGCTGTGAGA
36892_at	577	TCCCCTTAGAGTGCTGTGAGATGAG
36892_at	578	TCACCCTGTGTAACAGGACCCCAAG
36892_at	579	TCATCTGACCTTAGTTTGCTGCCAT
36892_at	580	CATCTGACCTTAGTTTGCTGCCATC
36892_at	581	ACCTTAGTTTGCTGCCATCAGTCTA
36892_at	582	TAGTTTGCTGCCATCAGTCTAGTGG
36892_at	583	AGTTTGCTGCCATCAGTCTAGTGGT
36892_at	584	TTGCTGCCATCAGTCTAGTGGTTTC
36892_at	585	CTGCCATCAGTCTAGTGGTTTCGTG
36892_at	586	TCAGTCTAGTGGTTTCGTGGTTTCG
36892_at	587	GTCTAGTGGTTTCGTGGTTTCGTCT
37152_at	588	AGGCCAAGGCTATGAAGGGACAGCT
37152_at	589	ATATTTTGTCTAGGAGCCCCAGCTT
37152_at	590	TATTTTGTCTAGGAGCCCCAGCTTC
37152_at	591	ATTTTGTCTAGGAGCCCCAGCTTCC
37152_at	592	GCTAGGAGCCCCAGCTTCCTGTGTT
37152_at	593	CTAGGAGCCCCAGCTTCCTGTGTTT
37152_at	594	TAGGAGCCCCAGCTTCCTGTGTTTT
37152_at	595	AGGAGCCCCAGCTTCCTGTGTTTTT
37152_at	596	GGAGCCCCAGCTTCCTGTGTTTTTA
37152_at	597	TAAATAGTGTACACAGACTGACGAA
37152_at	598	AATAGTGTACACAGACTGACGAAAC
37152_at	599	ATAGTGTACACAGACTGACGAAACT
37152_at	600	TAGTGTACACAGACTGACGAAACTT
37152_at	601	GTGTACACAGACTGACGAAACTTTA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37152_at	602	TGTACACAGACTGACGAAACTTTAA
37152_at	603	GTACACAGACTGACGAAACTTTAAA
37603_at	604	TGTGATGTCCCAACTTGTA AAAAATT
37603_at	605	TATGGTACTATGTTAGCCCCATAAT
37603_at	606	TGGTACTATGTTAGCCCCATAATTT
37603_at	607	ACTCCAGATTTTTTTACAGCTGCCTG
37603_at	608	CCAGATTTTTTTACAGCTGCCTGCAG
37603_at	609	TTACAGCTGCCTGCAGTACTTTACC
37603_at	610	GCAGTACTTTACCTCCTATCAGAAG
37603_at	611	TCTCAGCTCCCAAGGCTCTGAGCAA
37603_at	612	AGGCTCTGAGCAAATGTGGCTCCTG
37603_at	613	CTCTGAGCAAATGTGGCTCCTGGGG
37603_at	614	GGAAACATGACTCGTATATGTCTCA
37603_at	615	ATGACTCGTATATGTCTCAGGTCCC
37603_at	616	ATATGTCTCAGGTCCCTGCAGGGCC
37603_at	617	AAGCACCTAGCCTCGCTCTTGGCAG
37603_at	618	GTATATGTTGGGTGCAAAGTTCCCT
37603_at	619	TATATGTTGGGTGCAAAGTTCCCTA
37148_at	620	ACTTGTGGGACTCACCTGACTCAAA
37148_at	621	CTTGTGGGACTCACCTGACTCAAAG
37148_at	622	TTGTGGGACTCACCTGACTCAAAGA
37148_at	623	TGTGGGACTCACCTGACTCAAAGAT
37148_at	624	GTGGGACTCACCTGACTCAAAGATG
37148_at	625	TGGGACTCACCTGACTCAAAGATGA
37148_at	626	GGGACTCACCTGACTCAAAGATGAC
37148_at	627	GACTCACCTGACTCAAAGATGACTA
37148_at	628	CCTGACTCAAAGATGACTAATATCG
37148_at	629	CTGACTCAAAGATGACTAATATCGT
37148_at	630	AGATGACTAATATCGTCCCATTTTG
37148_at	631	GATGACTAATATCGTCCCATTTTGG
37148_at	632	ATGACTAATATCGTCCCATTTTGGGA
37148_at	633	TGACTAATATCGTCCCATTTTGGAA
37148_at	634	ATATCGTCCCATTTTGGAAATAAAG
37148_at	635	ATCGTCCCATTTTGGAAATAAAGCA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34740_at	636	CATGCATTAAGCTTGCAGTATTTTC
34740_at	637	AGCATCACAAGCTTTTGAGCGCATG
34740_at	638	GCGCATGGAAGCTCCATAAACTAACA
34740_at	639	TATGTGCACCCGTCCAGGACAGAAC
34740_at	640	ATGTGCACCCGTCCAGGACAGAACC
34740_at	641	ACCCGTCCAGGACAGAACCCTGCAT
34740_at	642	TGGAGCACAGCGTCCGGCCCAAGTGT
34740_at	643	CAAGTCTACGGGTGCCAGATCAGTA
34740_at	644	TACGGGTGCCAGATCAGTAGGGCCT
34740_at	645	TGCCAGATCAGTAGGGCCTGTGATT
34740_at	646	ATCAGTAGGGCCTGTGATTTCTGT
34740_at	647	TGTGATTTCTGTGAGTGTCTCAG
34740_at	648	TCAGTGTCTCAGCTAATGTGAACA
34740_at	649	TCCTCAGCTAATGTGAACAGTGTTG
34740_at	650	CAGTGTTGGTCTGCTGGTTAGAAAC
34740_at	651	GAAAGAAATCAGCTCAGCTCTCCAC
37747_at	652	CCTCTCTTTATTCCATGATTAAGGG
37747_at	653	AAGATGACTAACGTGTCACGGGGAA
37747_at	654	AGATGACTAACGTGTCACGGGGAAAG
37747_at	655	CGTGTCACGGGGAAAGAGCTCCCTGC
37747_at	656	CCTTTAGCTGCATTTGTATGCCAGT
37747_at	657	TGCCAGTGCTTAACACATTGCCTTA
37747_at	658	GCCAGTGCTTAACACATTGCCTTAT
37747_at	659	GACCAACACATACACGTCATAGAAG
37747_at	660	GGTGCTTCTTTCTGATCTCTAGTGG
37747_at	661	GATCTCTAGTGGAGATCTCTTTGAC
37747_at	662	AAGTTTAATGCCTGGCCATTTTCCA
37747_at	663	AGAGGCTAGAGTGCTTTTAGCCTTT
37747_at	664	GCTAGAGTGCTTTTAGCCTTTTTTA
37747_at	665	GTAACCATGATACTTTAATCAGAAG
37747_at	666	CTTAGCCTTGAAATTGTGAACTCTT
37747_at	667	GAAGTTCGCAACTAACTAAACCTG
36567_at	668	TTGGCCTTACCAGGTGACTTGCAAA
36567_at	669	GCCTTACCAGGTGACTTGCAAAGGG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36567_at	670	GTTTCAAATCTCTCCTTTCAGGGCT
36567_at	671	ATCTCTCCTTTCAGGGCTTTATTG
36567_at	672	TCCTTTCAGGGCTTTATTTGAATGG
36567_at	673	CTTTCAGGGCTTTATTTGAATGGAC
36567_at	674	TTATTTGAATGGACAGTTCGACCTC
36567_at	675	TATTTGAATGGACAGTTCGACCTCT
36567_at	676	TGAATGGACAGTTCGACCTCTTACT
36567_at	677	GGACAGTTCGACCTCTTACTCTCTC
36567_at	678	GTTCGACCTCTTACTCTCTCTTGTG
36567_at	679	GACCTCTTACTCTCTCTTGTGGTTT
36567_at	680	AAATTCAAGGTCCTCCTCTAGAAGT
36567_at	681	ATTCAAGGTCCTCCTCTAGAAGTTT
36567_at	682	CAAGGTCCTCCTCTAGAAGTTTCAA
36567_at	683	GGTCCTCCTCTAGAAGTTTCAAATC
38956_at	684	CGAACCAGACTCAGTGACCACGTCA
38956_at	685	AGACTCAGTGACCACGTCATGACAG
38956_at	686	AGTGACCACGTCATGACAGAACAGC
38956_at	687	CACGTCATGACAGAACAGCACATCC
38956_at	688	TTAAAGGGACGAGTCTGCCTTCCTG
38956_at	689	TCTACAGACCTCATCACTGGATTG
38956_at	690	GGATTTGCCAACTAGAATTGATTT
38956_at	691	TAGAATTCGATTTCTGTGCATAGGA
38956_at	692	TCCTGTGCATAGGAAGCTCCTTGGAA
38956_at	693	TGTTTACAGACCTGTTTTGTCATCC
38956_at	694	CAGACCTGTTTTGTCATCCTGCTGC
38956_at	695	TGTTTTGTCATCCTGCTGCCAAGAA
38956_at	696	GCTTGTTCCTCCACGGTCTGGCTTC
38956_at	697	CCCCTGTGGGGCAGCCAAGTTCCTG
38956_at	698	TGATAGCACTTGTGCCTCAGCCCCT
38956_at	699	AAGGGGCTGCCAACGAACCAGACTC
32207_at	700	CTCACTGGTCAATAATGGTGTGAT
32207_at	701	GAAATTACAAGAAGCCTTCGACCAA
32207_at	702	CAAGCGTGCAAGTCTCCACAGTGGG
32207_at	703	CTGTCTCCTGGGTTTACTAAGCTTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
32207_at	704	TAAGCTTGTAGAATGGGGGAACCCA
32207_at	705	GGGGGAACCCACTGTATGCCCTCT
32207_at	706	TCTCCAGCATTTGGAATTCCACCCG
32207_at	707	ACCCGCCTTGCTTTAAGACAAACAG
32207_at	708	CTTTAAGACAAACAGGGCTGCTCCA
32207_at	709	TGCTCCAAGTAGTTTTGTGTCAGCT
32207_at	710	GCTCCAAGTAGTTTTGTGTCAGCTT
32207_at	711	CCTAATTCAGCCAGTAAGGTTTCAGT
32207_at	712	GATGGGGCCCCACTGATCTGGATTT
32207_at	713	CCCACTGATCTGGATTTGAAAAGGA
32207_at	714	AGAAGTACTACCAAAATGTAAGTGC
32207_at	715	GAAGTACTACCAAAATGTAAGTGC
36791_g_at	716	CTGAGTTTGCGGAGAGGTCAGTAAC
36791_g_at	717	GCTCATGCCAAAGAAGAAAACCTTA
36791_g_at	718	AAACCTTAGTATGCATCAGATGCTG
36791_g_at	719	GACTTTACTGGAGTTAAACAACATG
36791_g_at	720	CAACATGTGAAAACCTCCTTAGCTG
36791_g_at	721	TGAAAACCTCCTTAGCTGCGACCAC
36791_g_at	722	GCTGCGACCACATTCTTTCATTTTG
36791_g_at	723	GAAACATCCACAAGATACCAGCTAG
36791_g_at	724	CAAGATACCAGCTAGGTCAGGGGGT
36791_g_at	725	CAAGCCCATGTCAGGGCGATCCTGG
36791_g_at	726	CATGTCAGGGCGATCCTGGTTCAAA
36791_g_at	727	AAATGTGCCATTTCCCGGGTTGATG
36791_g_at	728	CCATTTCCCGGGTTGATGCTGCCAC
36791_g_at	729	CCCGGGTTGATGCTGCCACACTTTG
36791_g_at	730	GCCACACTTTGTAGAGAGTTTAGCA
36791_g_at	731	AGAGTTTAGCAACACAGTGTGCTTA
31684_at	732	TACTATATCCAGCAAGACACTAAGG
31684_at	733	TATATCCAGCAAGACACTAAGGGTG
31684_at	734	AGACACTAAGGGTGCTGTACCTGTG
31684_at	735	GACACTAAGGGTGCTGTACCTGTGT
31684_at	736	ACACTAAGGGTGCTGTACCTGTGTG
31684_at	737	ACTAAGGGTGCTGTACCTGTGTGGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31684_at	738	AGATGGCTGAAGTCCGACACAGCAC
31684_at	739	CTGAAGTCCGACACAGCACGAGCGT
31684_at	740	CCTCATTTTAGTTGCCTAAGCATTG
31684_at	741	ATTTTAGTTGCCTAAGCATTGCCTG
31684_at	742	TTTCCTGAACCTGGTCCAGTGTATT
31684_at	743	CGCTGACCGGCTGTACGACTCCATA
31684_at	744	TCCATAATGGGCATGGGGACTCAAG
31684_at	745	CCATAATGGGCATGGGGACTCAAGA
31684_at	746	GAAAGTATAGCAAGTCCCTGTACTA
31684_at	747	AAAGTATAGCAAGTCCCTGTACTAC
1401_g_at	748	CCTGAAGGACTTTCTGCTTGTCATC
1401_g_at	749	AGGACTTTCTGCTTGTCATCCCCTT
1401_g_at	750	CTTTCTGCTTGTCATCCCCTTTGAC
1401_g_at	751	TTGTCATCCCCTTTGACTGCTGGGA
1401_g_at	752	AGCCGGGGAGCTGCTCTCTCATGAA
1401_g_at	753	GGAGCTGCTCTCTCATGAAACAAGA
1401_g_at	754	TGCTCTCTCATGAAACAAGAGCTAG
1401_g_at	755	ACAAGAGCTAGAAACTCAGGATGGT
1401_g_at	756	CTAGAAACTCAGGATGGTCATCTTG
1401_g_at	757	AACTCAGGATGGTCATCTTGGAGGG
1401_g_at	758	CAGGATGGTCATCTTGGAGGGACCA
1401_g_at	759	ATGGTCATCTTGGAGGGACCAAGGG
1401_g_at	760	GCCCTGGGCCACACTGACCCTGATA
1401_g_at	761	ACTGACCCTGATACAGGCATGGCAG
1401_g_at	762	GATACAGGCATGGCAGAAGAATGGG
1401_g_at	763	TTATTCAAGATGTTTTACCGTAATA
37542_at	764	CAGTTAATGCTAGTCTTTCATGTGA
37542_at	765	CCTTAGCTGTAAGAGTCTGGCTTAG
37542_at	766	GGCTTAGAACAGACCTCTCTGTGCA
37542_at	767	GAACAGACCTCTCTGTGCAATAACT
37542_at	768	CTCTGTGCAATAACTTGTGGCCACT
37542_at	769	TGCTCTGGAGGGACTCGGCACCACT
37542_at	770	GGACTCGGCACCACTTGATATTCAA
37542_at	771	GGCACCACTTGATATTCAACAGCCA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37542_at	772	TTGATATTCAACAGCCACTTGAGCC
37542_at	773	TTGTATTTACAGCTGATGGACTCAA
37542_at	774	TTACAGCTGATGGACTCAATTTGAG
37542_at	775	TGGACTCAATTTGAGCCTTCAAACCT
37542_at	776	GAGCCTTCAAACCTTGTAGTTATCCT
37542_at	777	ACATTGTCTAGCATTGATTTGGTTC
37542_at	778	CATTGTCTAGCATTGATTTGGTTCC
37542_at	779	CATTGATTTGGTTCCTGTGCATATG
37966_at	780	ATTCTAAACACTCGTGCTTGCGTTT
37966_at	781	TAAACACTCGTGCTTGCGTTTGAAG
37966_at	782	AACACTCGTGCTTGCGTTTGAAGCC
37966_at	783	CTCGTGCTTGCGTTTGAAGCCTCGC
37966_at	784	GTGCTTGCGTTTGAAGCCTCGCGTC
37966_at	785	TGCTTGCGTTTGAAGCCTCGCGTCA
37966_at	786	GCTTGCGTTTGAAGCCTCGCGTCAC
37966_at	787	GCGTTTGAAGCCTCGCGTCACTCAG
37966_at	788	TGAAGCCTCGCGTCACTCAGTCGCG
37966_at	789	AAGCCTCGCGTCACTCAGTCGCGTG
37966_at	790	TGTTGTCTGCCTTGGCCGAAAGATG
37966_at	791	CTGCCTTGGCCGAAAGATGAAAAAA
37966_at	792	ATTCACCGGGGATCTCCTGGGCTGG
37966_at	793	GCTCTCCTTGGGAAGTGAGGCCTTTT
37966_at	794	TCTCCTTGGGAAGTGAGGCCTTTTAT
37966_at	795	TCCTTGGGAAGTGAGGCCTTTTATTA
38784_g_at	796	GTCTGTGTTCTGGTTGCGCTGGCCA
38784_g_at	797	CTGTGTTCTGGTTGCGCTGGCCATT
38784_g_at	798	TTCTGGTTGCGCTGGCCATTGTCTA
38784_g_at	799	GCGCTGGCCATTGTCTATCTCATTG
38784_g_at	800	GCCATTGTCTATCTCATTGCCTTGG
38784_g_at	801	GGCTGTCTGTCTAGTGCCGCCGAAAG
38784_g_at	802	GCTGTCTGTCTAGTGCCGCCGAAAGA
38784_g_at	803	TCAGTGCCGCCGAAAGAACTACGGG
38784_g_at	804	CCGCCGAAAGAACTACGGGCAGCTG
38784_g_at	805	GAACCTACGGGCAGCTGGACATCTTT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38784_g_at	806	CGGGCAGCTGGACATCTTTCCAGCC
38784_g_at	807	GGACATCTTTCCAGCCCGGGATACC
38784_g_at	808	AGCCCGGGATACCTACCATCCTATG
38784_g_at	809	GCCCGGGATACCTACCATCCTATGA
38784_g_at	810	ACCTACCATCCTATGAGCGAGTACC
38784_g_at	811	TACCATCCTATGAGCGAGTACCCCA
40331_at	812	ACAAGCTGGCCAGAAGGGAGACCAG
40331_at	813	AGGTGAAAACCTCAGTGTCCGTCAGG
40331_at	814	AGGCCGGGCTGAAGTTTACTACAGT
40331_at	815	CCCTGTACAAAGTGGGAGCTGGCAC
40331_at	816	CGGAGAGTACCCTGTGGAGCTGCAC
40331_at	817	GGAGAGTACCCTGTGGAGCTGCACC
40331_at	818	GTACCCTGTGGAGCTGCACCAAGAA
40331_at	819	CCCTGTGGAGCTGCACCAAGAATAG
40331_at	820	TGTGGAGCTGCACCAAGAATAGCTG
40331_at	821	GCACCAAGAATAGCTGGGGCCATCA
40331_at	822	ATAGCTGGGGCCATCATGACTGCAG
40331_at	823	GTGCAGCGTCTGACCCGGAAACCCT
40331_at	824	GTGTCCTCGGGCTCATATGTGGGAA
40331_at	825	GCAGAGGATCTCTGAGGAGTTCCCT
40331_at	826	TGAGGAGTTCCCTGGGGACAACCTGA
40331_at	827	GGACAACCTGAGCAGCCTCTGGAGAG
40371_at	828	TAAATACCAGACTGCAGGTTGGACC
40371_at	829	TTACAGCTCCCCAAGTGGTTTCCAC
40371_at	830	GGTTTCCACATGCTCTGAGAAGAGG
40371_at	831	CCCTCATCTTGAAGGGCCCAGGAGG
40371_at	832	GAGAGGAACTCCTTGGCCTAGCCCA
40371_at	833	TGCTGCCTTCTGACGGCCCTGCAAT
40371_at	834	CACATGCTGGCCAGCCTGGGGCCTG
40371_at	835	GAGGTCAGGCCCTGGAACCTCTATCT
40371_at	836	GTCAGGCCCTGGAACCTCTATCTGGG
40371_at	837	CTGGAACCTCTATCTGGGCCTGGGCT
40371_at	838	TGGAACCTCTATCTGGGCCTGGGCTA
40371_at	839	GGACATCAGAGGTTCTTTGAGGGAC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40371_at	840	GACATCAGAGGTTCTTTGAGGGACT
40371_at	841	GAGGGACTGCCTCTGCCACACTCTG
40371_at	842	AGGGACTGCCTCTGCCACACTCTGA
40371_at	843	TTCCACTGCCTCTGCCTTAGAGGAG
32339_at	844	CCCGCTGGACTTATAATGCCACCTT
32339_at	845	CCGCTGGACTTATAATGCCACCTTC
32339_at	846	CTGGACTTATAATGCCACCTTCTGT
32339_at	847	TGCACCCTTGGCTCTGGCCAAAGCT
32339_at	848	GCACCCTTGGCTCTGGCCAAAGCTT
32339_at	849	ACCTGCGTGGCTCTGTTACTACAGC
32339_at	850	CTGCGTGGCTCTGTTACTACAGCCA
32339_at	851	GCGTGGCTCTGTTACTACAGCCACT
32339_at	852	GTGGCTCTGTTACTACAGCCACTGC
32339_at	853	TGGCTCTGTTACTACAGCCACTGCT
32339_at	854	GGCTCTGTTACTACAGCCACTGCTG
32339_at	855	CTCTGTTACTACAGCCACTGCTGGG
32339_at	856	GTTACTACAGCCACTGCTGGGTGCC
32339_at	857	TTACTACAGCCACTGCTGGGTGCC
32339_at	858	ACTACAGCCACTGCTGGGTGCCAG
32339_at	859	TACAGCCACTGCTGGGTGCCAGGG
34435_at	860	CTAGCCAGAAGTGGAATTGGCAGCT
34435_at	861	AATTGGCAGCTTCTAGAATATGTAC
34435_at	862	GGACAAAATGTTCTCAATCTTAAG
34435_at	863	ATACAAAGACCCTCATTGTCTGGGT
34435_at	864	TCCACACTTACTGAGTACAGATGA
34435_at	865	AACATTACATTCAGGGGATTTCCTC
34435_at	866	GGCTCAGTCTTTTCCCCTTGAAGTT
34435_at	867	TCCCCTTGAAGTTCTCTAATAGATG
34435_at	868	CTTGAAGTTCTCTAATAGATGTTAC
34435_at	869	ATGTTACTTTTGACAAAAGATCGCC
34435_at	870	GTCAAAGTGTCAAAAAGCCCAGAAT
34435_at	871	CCCAGAATTCCCAAAGGCATTAGGT
34435_at	872	GCTGATATCAGAACAGCAGAAATTA
34435_at	873	ATGTTTCTGATGACTTATGTTCTAC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34435_at	874	CAATCTATGGACATACGGGATTTTT
34435_at	875	TTTTCTTGCTTTGAAGCTACCTGGA
37136_at	876	CACGGCCAGTGTACGTACAGCATC
37136_at	877	TGTCACGTACAGCATCTGTGGTTCC
37136_at	878	TCACGTACAGCATCTGTGGTTCCAG
37136_at	879	ACAGCATCTGTGGTTCCAGTCTGTG
37136_at	880	CATCTGTGGTTCCAGTCTGTGCTTG
37136_at	881	TGTGGTTCCAGTCTGTGCTTGACAT
37136_at	882	CCATCCCACTGGAGTCAGGGGGGCTC
37136_at	883	CATCCCACTGGAGTCAGGGGGGCTCG
37136_at	884	ATCACCTTCGCAGCTATGTGCGGG
37136_at	885	TCACCCTTCGCAGCTATGTGCGGGC
37136_at	886	GCAACAGCGCCGAGCGCCTGCTGGA
37136_at	887	GCGCGCGCCGTGGAGAACCAGTACT
37136_at	888	CGCGCCGTGGAGAACCAGTACTCCT
37136_at	889	GTGGAGAACCAGTACTCCTTCTACT
37136_at	890	GAGAACCAGTACTCCTTCTACTAGC
37136_at	891	GTGGGACACGCCAAGCTCTTCAGTG
37285_at	892	CTCTAGAATCTGTGCGGCTGCTCAA
37285_at	893	CAATGCAGCACTCAACAGCAAGCTC
37285_at	894	AGCACTCAACAGCAAGCTCTGTGAT
37285_at	895	GTGATCTCCTGCTCTCCAAGCATGG
37285_at	896	GGTGAAGAGCTCCTGCGCTTGGCAC
37285_at	897	CCACAGCCCTCAGATGATGGAAGAT
37285_at	898	ATTTTGTGGAGAAGCTGCTGCTGGC
37285_at	899	CTGTCGCCGTCCTGTACACTTTGAG
37285_at	900	GTACACTTTGAGCTCATGAGTGAGT
37285_at	901	CTACTTCGGGAACATGGGGCCCCAG
37285_at	902	GGGGCCCCAGTATGTCACCACCTAT
37285_at	903	GTATGTCACCACCTATGCCTGAGAA
37285_at	904	CTGAGAAGCCAGCTGCCTAGGATTC
37285_at	905	CAGGCCTACTCCTGTCTTCTGCTTT
37285_at	906	TTGTTGTGTGCCTCTAGCTGAATTG
37285_at	907	GCCTCTAGCTGAATTGAGCCTAAAA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37391_at	908	TTTCTGTTGCTATTGATGCAGGTCA
37391_at	909	TTGATGCAGGTCATGAGTCCTTCCT
37391_at	910	CAGGTCATGAGTCCTTCCTGTTCTA
37391_at	911	CATGAGTCCTTCCTGTTCTATAAAG
37391_at	912	ATGAGTCCTTCCTGTTCTATAAAGA
37391_at	913	AGTCCTTCCTGTTCTATAAAGAAGG
37391_at	914	TTTGAGCCAGACTGTAGCAGTGAAG
37391_at	915	CCAGACTGTAGCAGTGAAGACATGG
37391_at	916	CCAAAGACCGGAGAAACCATTGTGG
37391_at	917	ACCGGAGAAACCATTGTGGAATTGC
37391_at	918	GAAACCATTGTGGAATTGCCTCAGC
37391_at	919	ATGGCGCATGCATGGGAGGAATTCA
37391_at	920	GAGGAATTCATCTTCAGTCTACCAG
37391_at	921	GGAATTCATCTTCAGTCTACCAGCC
37391_at	922	CCGCTGTGTCGGATACACACTCGAA
37391_at	923	CGCTGTGTCGGATACACACTCGAAT
35692_at	924	GTGGGCGTTTCTTCTTGTACTTATG
35692_at	925	GGGCGTTTCTTCTTGTACTTATGTG
35692_at	926	CTCTTCCCGAGATGGGGCCGCCGAG
35692_at	927	TGCTGCGCTTCCAGTTCCGAAAAGC
35692_at	928	TGTTTAAGCCCTTGGACTGAGGGTG
35692_at	929	ATCGCAGCTCCGAAGACGGAGAGGA
35692_at	930	ACCCACGTGCCCTAGATTCATGGCA
35692_at	931	GCCCTAGATTCATGGCAGAAAATGA
35692_at	932	TAGATTCATGGCAGAAAATGACCAA
35692_at	933	CAGAAAATGACCAAATCCTGTGTAT
35692_at	934	AATGACCAAATCCTGTGTATTTGTT
35692_at	935	GCTATTGCTGTAGTAAGAGAAGCTC
35692_at	936	AAGAGAAGCTCTTTGTATCTGAACA
35692_at	937	AGAAGCTCTTTGTATCTGAACATAG
35692_at	938	AGCTCTTTGTATCTGAACATAGTTG
35692_at	939	CTCTTTGTATCTGAACATAGTTGTA
38449_at	940	GTCAGCCAGGCCTGCCAGGTCTTCA
38449_at	941	CAGGACAGGTGTCCTGGCCTTTCTT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38449_at	942	GTGTCCTGGCCTTTCTTCCTGAGGT
38449_at	943	GCCTTTCTTCCTGAGGTCTCTAGGG
38449_at	944	TTTCTTCCTGAGGTCTCTAGGGGAG
38449_at	945	GATTATGTCTGCTGTCATGTCTGGG
38449_at	946	CATGTCTGGGTCTTTAGGGTAGGAC
38449_at	947	AGGCAGGAGTCTCCACAAGGCTTCA
38449_at	948	ACAAGGCTTCATGTGGCCCCTTATA
38449_at	949	GGAAGGTCCCTTCATGCTGGAGGCA
38449_at	950	CACACAGCTTTAAGGAAGTAGGTTG
38449_at	951	GTTGAAGTAGGACTCCTTCGTCCTC
38449_at	952	TAGGACTCCTTCGTCCTCTCACTGG
38449_at	953	CTTCGTCCTCTCACTGGCTTTGGCT
38449_at	954	TTCGTCCTCTCACTGGCTTTGGCTC
38449_at	955	TCTCACTGGCTTTGGCTCCCTCAAT
37002_at	956	CCCACGTGGTAGTGGGAGATGTTCT
37002_at	957	AGCCGATGTGGACAAGACCGTGGCT
37002_at	958	GCAATGACCTCAGTCCCACGACAGT
37002_at	959	ATGCACAAGGTGCTGCGGGAATCAG
37002_at	960	ATGCCGCCACACATAGGAGACCAGC
37002_at	961	CACATAGGAGACCAGCCACTAACTG
37002_at	962	TCAAGGGTCATCTCCAAACATGACC
37002_at	963	GTCATCTCCAAACATGACCTGGGCC
37002_at	964	CCAAACATGACCTGGGCCATTTCAT
37002_at	965	GCCTCACCACCGATGAGTACGACGG
37002_at	966	ACCGATGAGTACGACGGACACAGCA
37002_at	967	GAGTACGACGGACACAGCACCTACC
37002_at	968	AGTACCAGTAGCACTCTGTCCCCAT
37002_at	969	AGTAGCACTCTGTCCCCATCTGGGA
37002_at	970	CATTCTGGGACATGAGGAGCAAAGG
37002_at	971	TGTTGAGCCAAGAGCTTCAAATTAC
1139_at	972	GACCAGCAACAGAAGCCCTTATACC
1139_at	973	ACTGCTATCAACACGGAGAACATCC
1139_at	974	GATACTATTCTGCATGACAACCTCA
1139_at	975	ATTCTGCATGACAACCTCAAGCAGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1139_at	976	CATGACAACCTCAAGCAGCTTATGC
1139_at	977	AACCTCAAGCAGCTTATGCTACAGT
1139_at	978	TCTGCGGCCTTTGGTTTGTGGCTGA
1139_at	979	GCCTTTGGTTTGTGGCTGAAAGCTG
1139_at	980	GTTGAGTGACTCATCGCCAAGATTT
1139_at	981	TGACTCATCGCCAAGATTTGCTGTA
1139_at	982	ATCGCCAAGATTTGCTGTAATGCAG
1139_at	983	GAAGATCGACTGACCAATCGCCTTA
1139_at	984	CGCCTTACAGAGTCTCTGAACATTT
1139_at	985	ACAGAGTCTCTGAACATTTTGTAAA
1139_at	986	TCTCTGAACATTTTGTAAACAATCG
1139_at	987	GTTTTTCAGCAATGTCTCCATAATTC
1622_at	988	CCTAGGGTACCAGCAGGCAGAGCCT
1622_at	989	TAGGGTACCAGCAGGCAGAGCCTTG
1622_at	990	GTACCAGCAGGCAGAGCCTTGCCCT
1622_at	991	GCAGAGCCTTGCCCTCTGCTCAGGC
1622_at	992	GAGGGGCCCAAAATCTCTGCTCAGA
1622_at	993	GGCCCAAAATCTCTGCTCAGAGAAG
1622_at	994	CCCAAAATCTCTGCTCAGAGAAGTG
1622_at	995	AAATCTCTGCTCAGAGAAGTGCAGG
1622_at	996	ATCTCTGCTCAGAGAAGTGCAGGGG
1622_at	997	CTCACTCTCCCTGAGGACTGGCGTG
1622_at	998	CACTCTCCCTGAGGACTGGCGTGAC
1622_at	999	CTCTCCCTGAGGACTGGCGTGACAG
1622_at	1000	CTCCCTGAGGACTGGCGTGACAGGG
1622_at	1001	GGGGCAGTTACCTGGTTGCTGTTTT
1622_at	1002	GGCAGTTACCTGGTTGCTGTTTTAA
1622_at	1003	CAGTTACCTGGTTGCTGTTTTAATT
32606_at	1004	GAGAATGTTTGTCACTCCCAAAAAT
32606_at	1005	CCCAAAAATATCTGGAGAGGAAGAA
32606_at	1006	GATTGGCATTGAGATCCATGTGGAC
32606_at	1007	CTGTCTGAAAGCTGGCATTTCATCA
32606_at	1008	ACTGCTCTCATAAAGATCTGATTGC
32606_at	1009	CTCTCATAAAGATCTGATTGCCTTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
32606_at	1010	CCCAACTCCCATTGCAGAAGAAAAG
32606_at	1011	TCCCATTGCAGAAGAAAAGCTATTC
32606_at	1012	AAAGCTATTCAACTCTCAGCGGTGG
32606_at	1013	AGCTATTCAACTCTCAGCGGTGGAG
32606_at	1014	CAGACGCGGATCTTGGAAATCCAGG
32606_at	1015	ATCTTGGAAATCCAGGACTTCTTGG
32606_at	1016	ACAGAACTACAGGTGCACCCAACCA
32606_at	1017	TCCCTTGATGGGACAACATCCTGTA
32606_at	1018	AGGTGCACCCAACCACGGACATGCA
32606_at	1019	CTCGTCATGAGAAATCTAGGTAGGC
39436_at	1020	CCTAACAGAGTTTACTGTTGTTTAG
39436_at	1021	ATTTGCAAGGGCTTCTTTTCCGCAA
39436_at	1022	TTGCAAGGGCTTCTTTTCCGCAAAT
39436_at	1023	CTAATTAGTGCCACCAGACTAGACC
39436_at	1024	AATTAGTGCCACCAGACTAGACCTG
39436_at	1025	TAGTGCCACCAGACTAGACCTGTAT
39436_at	1026	TGCCACCAGACTAGACCTGTATCAT
39436_at	1027	CAGACTAGACCTGTATCATTTCATGG
39436_at	1028	AGACCTGTATCATTTCATGGTATAAA
39436_at	1029	GACCTGTATCATTTCATGGTATAAAT
39436_at	1030	ATCTCTCTCTTAAAACGAGATCAGG
39436_at	1031	TCTCTTAAAACGAGATCAGGTTAGC
39436_at	1032	TTATACCCTTTTTGGCCTGAAGACA
39436_at	1033	CCTTTTTGGCCTGAAGACATTTTAG
39436_at	1034	TGGCCTGAAGACATTTTAGAATTTC
39436_at	1035	TAGAATTTCTTAACAGAGTTTACTG
40274_at	1036	AGGGTTCTCTGTGTGTGTCCCCGGC
40274_at	1037	GGTTCTCTGTGTGTGTGTCCCCGGCAC
40274_at	1038	GTTCTCTGTGTGTGTGTGTCCCCGGCACG
40274_at	1039	TTCTCTGTGTGTGTGTGTGTCCCCGGCACGT
40274_at	1040	TCTCTGTGTGTGTGTGTGTGTCCCCGGCACGTC
40274_at	1041	CGCCTCCGTTAACACGATCCTGAAT
40274_at	1042	GCCTCCGTTAACACGATCCTGAATA
40274_at	1043	AACACGATCCTGAATAAATCTTGAG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40274_at	1044	CACGATCCTGAATAAATCTTGAGAA
40274_at	1045	ACGATCCTGAATAAATCTTGAGAAC
40274_at	1046	CGATCCTGAATAAATCTTGAGAACC
40274_at	1047	GATCCTGAATAAATCTTGAGAACCC
40274_at	1048	AGGGCAGCTCCCTGGCATACTGGCT
40274_at	1049	GCATACTGGCTGCAGCCCGTGGGCA
40274_at	1050	CATACTGGCTGCAGCCCGTGGGCAG
40274_at	1051	GCAGCTCCGGGCTGTTCGTCCATAGA
37945_at	1052	GCCACTGGTGCCTCGAGTAGCCATG
37945_at	1053	TGTCCAGTCACTTAGAAGTTCCCCC
37945_at	1054	GGCCAAAACCCAATTCACATTGAG
37945_at	1055	TCTGAAGTTTTTCGTATCACAGTGTT
37945_at	1056	GTGTTAACCTGTACTCTCTCCTGCA
37945_at	1057	ATTCCAGTATCAATGCTACACAGTG
37945_at	1058	AATGCTACACAGTGTTGTCCCGAGC
37945_at	1059	GCGTTGGGCAGAAACCCTCGGGAAT
37945_at	1060	CACGCTGTAGGGTATGGGAAGAACC
37945_at	1061	CTAATAAAGCTGCTGCTTGGCTGGA
37945_at	1062	AAAGCTGCTGCTTGGCTGGAAAAA
37945_at	1063	TTGGGGCTCCCGTGGACAGTCTCAG
37945_at	1064	GGGGCTCCCGTGGACAGTCTCAGCC
37945_at	1065	ACCAGCACCTGCATGTACCCTAGAA
37945_at	1066	CACCGATTGGTGTCCGGCTGGTGAC
37945_at	1067	TCCCTGGTTTGGTGTCTTGGCCCCA
34255_at	1068	GCCCATGCTTCGACGGGGCAGCAGC
34255_at	1069	CAGCAGCAAGTGGATGGCCAGGACA
34255_at	1070	AGCCAATAGCCGTCCTCATGTACGT
34255_at	1071	TAGCCGTCCTCATGTACGTCCACGA
34255_at	1072	GTCTCATGTACGTCCACGACTACT
34255_at	1073	TCATGTACGTCCACGACTACTACGT
34255_at	1074	GTCCACGACTACTACGTGCTCAACT
34255_at	1075	CACGACTACTACGTGCTCAACTATG
34255_at	1076	CTACGTGCTCAACTATGAGGCCCCA
34255_at	1077	GTGCTCAACTATGAGGCCCCAGCGG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34255_at	1078	TGCTCAACTATGAGGCCCCAGCGGC
34255_at	1079	CTATGAGGCCCCAGCGGCAGAGGCC
34255_at	1080	CGGCAGAGGCCTGAGCTGCACCTGA
34255_at	1081	CACCTGAGGGCCTGGCTTCTCACTG
34255_at	1082	TGAGGGCCTGGCTTCTCACTGCCAC
34255_at	1083	CTCCTAGGCCTCGAGTGCTGGGGAT
905_at	1084	GCCGTGCAGGCCATGAACCGCATCT
905_at	1085	ATGAACCGCATCTGTGTGCTGGACG
905_at	1086	GATCTGCGGCCCATCTACATCTCTG
905_at	1087	CGGCCCATCTACATCTCTGTGCAGC
905_at	1088	CCGCCTTCACTGCACGTGCTGGAGC
905_at	1089	CTGCGGCAGCGCAACACTGAAACCG
905_at	1090	CTGTTTGATGTGGTCATCATTACG
905_at	1091	GACAGCCTGGACCAGGCCTACGCAG
905_at	1092	CTGGACCAGGCCTACGCAGAGCTGA
905_at	1093	GCGCTCTCTGAGGAAATCAAGAAAG
905_at	1094	GGCGCCTGAGGCTTGCTGTCTGTTC
905_at	1095	TACAGGACCAGGGCAGCAGCATTGA
905_at	1096	ACCAGGGCAGCAGCATTGAGCCACC
905_at	1097	CGATACGGCAGCTCTGTGCCCTTGG
905_at	1098	GGCAGCTCTGTGCCCTTGGCCAGCA
905_at	1099	CTCACTCTGGACCCAGGGCTGACAT
1569_r_at	1100	GTCGTGTGCTTGGAGGAAGCCGCGG
1569_r_at	1101	CGTGTGCTTGGAGGAAGCCGCGGAA
1569_r_at	1102	GAAGCCGCGGAACCCCCAGCGTCCG
1569_r_at	1103	CCCAGCGTCCGTCCATGGCGTGGAG
1569_r_at	1104	CGTCCATGGCGTGGAGCCTTGGGAG
1569_r_at	1105	CCATGGCGTGGAGCCTTGGGAGCTG
1569_r_at	1106	ATGGCGTGGAGCCTTGGGAGCTGGC
1569_r_at	1107	GGCGTGGAGCCTTGGGAGCTGGCTG
1569_r_at	1108	GCGTGGAGCCTTGGGAGCTGGCTGG
1569_r_at	1109	GTGGAGCCTTGGGAGCTGGCTGGGT
1569_r_at	1110	GGAGCCTTGGGAGCTGGCTGGGTGG
41125_r_at	1111	GACCCCAAATCCTGACCATATTAAT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
41125_r_at	1112	CCCCAAATCCTGACCATATTAATGC
41125_r_at	1113	CAAATCCTGACCATATTAATGCCCC
41125_r_at	1114	AATCCTGACCATATTAATGCCCCTG
41125_r_at	1115	ATCCTGACCATATTAATGCCCCTGA
41125_r_at	1116	TCCTGACCATATTAATGCCCCTGAA
41125_r_at	1117	CCTGACCATATTAATGCCCCTGAAT
41125_r_at	1118	ACCATATTAATGCCCCTGAATGACC
41125_r_at	1119	CCATATTAATGCCCCTGAATGACCC
41125_r_at	1120	ATATTAATGCCCCTGAATGACCCCC
41125_r_at	1121	TATTAATGCCCCTGAATGACCCCCC
41125_r_at	1122	TTAATGCCCCTGAATGACCCCCCAC
41125_r_at	1123	TAATGCCCCTGAATGACCCCCCACT
41125_r_at	1124	ATGCCCCTGAATGACCCCCCACTGT
41125_r_at	1125	TGCCCCTGAATGACCCCCCACTGTT
41125_r_at	1126	GCCCCTGAATGACCCCCCACTGTTT
35256_at	1127	CCTTTGAAGTAAGTGGCTAGAAACA
35256_at	1128	TGGCTAGAAACAGCACTCTGGTTAT
35256_at	1129	TATAATTGCCCCAGGGCCTGATTCA
35256_at	1130	CATAAACTGGAAGCTGCTTCCCCT
35256_at	1131	GTGAGCCCCTATTATTACTTTCAGA
35256_at	1132	TTCAGATTGTCTGTGACACTCAAGC
35256_at	1133	ATGTGGATCCAAGAAACCAGGGCCA
35256_at	1134	ATCCAAGAAACCAGGGCCATGACCA
35256_at	1135	CAGGTCCACTGTGGAGCAGCCATCT
35256_at	1136	GAGCAGCCATCTATCTACCTGACTC
35256_at	1137	GCCATCTATCTACCTGACTCCTGAG
35256_at	1138	TATCTACCTGACTCCTGAGCCAGGC
35256_at	1139	ATCTACCTGACTCCTGAGCCAGGCT
35256_at	1140	GCCAGGCTGCCGTGGTGTCAATTTCT
35256_at	1141	CCGTGCTCTGTTTCCTTTTGGAGTT
35256_at	1142	TCTCCACATTATCTTTGTTTCCTGGG
290_s_at	1143	GTGATGTCTAGCTGAGTCTTCATGA
290_s_at	1144	CCTGATTACTACAGAATTCCAGAAT
290_s_at	1145	CCTACTATTCAGAGACAACAGTGAC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
290_s_at	1146	GACCTATGTGATGCTGGCCTTAGTG
290_s_at	1147	CCTGACCACATGTGGCGTGGTTTAT
290_s_at	1148	CGTGGTTTATCCACTCTCCAAGAAC
290_s_at	1149	TCTCCAAGAACCATCTGGTAGTTCT
290_s_at	1150	AGTTCTGGCCATTGCCTTCTTCATG
290_s_at	1151	ATCATGCTGCAGCTCTACGCCCAA
290_s_at	1152	CCATGCCCAGCAGATTGCCCTTCAG
290_s_at	1153	CCGCAAGGGCATTGCCACACTGGCC
290_s_at	1154	TGCTTGAGCCTTTGCCGCCTGCTG
290_s_at	1155	CTGGTTGCCCTTCACTGTCTACTGC
290_s_at	1156	TGTCTACTGCCTGCTGGGTGATGCC
290_s_at	1157	CCTTCCGCAACCAGGATGTGCAGAA
290_s_at	1158	GCTGCTGCTGTTCTCTTCCAAGAT
34666_at	1159	AATATTCCATCCATATACTTTGGGG
34666_at	1160	TACTTTGGGGACTTGTAGGGATGCC
34666_at	1161	ACTTTGGGGACTTGTAGGGATGCCT
34666_at	1162	TGTAGGGATGCCTTTCTAGTCCTAT
34666_at	1163	GGATGCCTTTCTAGTCCTATTCTAT
34666_at	1164	TAGTCCTATTCTATTGCAGTTATAG
34666_at	1165	CCAAGGGAAACACTCGGCTTTCTAT
34666_at	1166	CTCGGCTTTCTATAGAAAATTGCAC
34666_at	1167	AAATTGCACTTTTTGTGAGTAATC
34666_at	1168	CTGGTAGATGTCACCCAGTGGTTTT
34666_at	1169	TCAAATGTTCTGTATAGTTTTTGC
34666_at	1170	TGCTCTATTGTAGCATTCTTGATG
34666_at	1171	CTATTGTAGCATTCTTGATGTTGC
34666_at	1172	GCATTCTTGATGTTGCTTAGTCAC
34666_at	1173	CATTCTTGATGTTGCTTAGTCACT
34666_at	1174	GATGTTGCTTAGTCACTTATTTTAT
34689_at	1175	GTGAAGGACCCTGGAGCCCTATCCA
34689_at	1176	GGTCTGCTGGCCATCCTGACCTTGG
34689_at	1177	GTCTGCTGGCCATCCTGACCTTGGC
34689_at	1178	CAGTAGCCACACTGTATGGACTATC
34689_at	1179	AGCCACACTGTATGGACTATCCCTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34689_at	1180	CCACACTGTATGGACTATCCCTGGC
34689_at	1181	ATCCCTGGCCACACCTGGGGAGTAG
34689_at	1182	CCCTGGCCACACCTGGGGAGTAGGC
34689_at	1183	CCACACCTGGGGAGTAGGCCAAGAA
34689_at	1184	GAGCGAGCAAGCAGCCCCTCAGAAC
34689_at	1185	CTAGGCAGCATCTACACTCGCCTGT
34689_at	1186	TACACTCGCCTGTATGGGCAGTCCC
34689_at	1187	AGTGGAGACCACAGGCCCTGCTGCG
34689_at	1188	TGGGTGGATGCTCACGCCAGGCCTT
34689_at	1189	AGACCATCTGCTGTCACAACCACTG
34689_at	1190	ACCTGGCCACAACCAGGAACACTAG
2090_i_at	1191	TGCGTAGTACAGTGCCACCGCTGCC
2090_i_at	1192	GCGTAGTACAGTGCCACCGCTGCCG
2090_i_at	1193	CGTAGTACAGTGCCACCGCTGCCGT
2090_i_at	1194	GTAGTACAGTGCCACCGCTGCCGTG
2090_i_at	1195	TAGTACAGTGCCACCGCTGCCGTGT
2090_i_at	1196	AGTACAGTGCCACCGCTGCCGTGTG
2090_i_at	1197	GTACAGTGCCACCGCTGCCGTGTGC
2090_i_at	1198	TACAGTGCCACCGCTGCCGTGTGCG
2090_i_at	1199	ACAGTGCCACCGCTGCCGTGTGCGC
2090_i_at	1200	CAGTGCCACCGCTGCCGTGTGCGCA
2090_i_at	1201	AGTGCCACCGCTGCCGTGTGCGCAA
37412_at	1202	CATCGACGTCTATGGAATTAAGTGC
37412_at	1203	TTAAGTGCCATGAAAACCTCGCCTAG
37412_at	1204	TGAAAACCTCGCCTAGGAAGGAGGTG
37412_at	1205	CTCGCCTAGGAAGGAGGTGTACTTC
37412_at	1206	AACCCAGAACAGTATTCAAAGCGCT
37412_at	1207	AGCGCTTTTTGGACTTTATTGGCCA
37412_at	1208	TGGCCACATCTTGACGTAACCTCCT
37412_at	1209	ATGAAAACCAAACCTCAGTGAAGTAC
37412_at	1210	TCAGTGAAGTACTCATCTTGACAGGA
37412_at	1211	CAGTGAAGTACTCATCTTGACAGGAA
37412_at	1212	ACTCATCTTGACAGGAAGCAAACCTC
37412_at	1213	CAGGAAGCAAACCTCCTTGTTTACA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37412_at	1214	TTGTTTACATCTTCAGGCCAAGATG
37412_at	1215	ATCTTCAGGCCAAGATGACTGATTT
37412_at	1216	CTTCAGGCCAAGATGACTGATTTGG
37412_at	1217	AGATGACTGATTTGGGGGCTACTCG
39799_at	1218	GTCATGAACAATGTCACCTGTACTC
39799_at	1219	CTGTACTCGGATCTATGAAAAAGTA
39799_at	1220	AAATTCCATCATCACTTTGGACAGG
39799_at	1221	AATTCCATCATCACTTTGGACAGGA
39799_at	1222	AGAATGACCAAGCTCAGTTCAATGA
39799_at	1223	ACCAAGCTCAGTTCAATGAGCAAAT
39799_at	1224	GTTCAATGAGCAAATCTCCATACTG
39799_at	1225	TTTTACATGCAGCTATTTCAAAGTG
39799_at	1226	TAGGATCATCCCTTTGGTTAATAAA
39799_at	1227	TATTGAGATGACACTCTAGCAATTT
39799_at	1228	TTGAGATGACACTCTAGCAATTTAT
39799_at	1229	TGAGATGACACTCTAGCAATTTATA
39799_at	1230	ATAGATAGCTACTCTTACAGGAAAT
39799_at	1231	GATAGCTACTCTTACAGGAAATACT
39799_at	1232	GCTACTCTTACAGGAAATACTGTAC
39799_at	1233	AGACCATTCTCAATAAAAGGTGACT
31859_at	1234	TTTCTTCTTCTCTGGGCGCCAGGTG
31859_at	1235	CCAGCGAGGTGGACCGGATGTTCCC
31859_at	1236	CCCGGGGTGCCTTTGGACACGCACG
31859_at	1237	CACGACGTCTTCCAGTACCGAGAGA
31859_at	1238	TCCAGTACCGAGAGAAAGCCTATTT
31859_at	1239	CAGTACCGAGAGAAAGCCTATTTCT
31859_at	1240	AGAGAAAGCCTATTTCTGCCAGGAC
31859_at	1241	TATTTCTGCCAGGACCGCTTCTACT
31859_at	1242	CTACTGGCGCGTGAGTTCCCGGAGT
31859_at	1243	GTGAGTTCCCGGAGTGAGTTGAACC
31859_at	1244	TGAGTTCCCGGAGTGAGTTGAACCA
31859_at	1245	TGAGTTGAACCAGGTGGACCAAGTG
31859_at	1246	TTGAACCAGGTGGACCAAGTGGGCT
31859_at	1247	GACCAAGTGGGCTACGTGACCTATG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31859_at	1248	ACCAAGTGGGCTACGTGACCTATGA
31859_at	1249	GTGGGCTACGTGACCTATGACATCC
37661_at	1250	AGATAAACAGTAACTCAGCGTAAGT
37661_at	1251	CGTAAGTGACCTGTGGATCATCAGT
37661_at	1252	TGACCTGTGGATCATCAGTAGTACC
37661_at	1253	GACCTGTGGATCATCAGTAGTACCC
37661_at	1254	GCTTTAGTTTATCTCAGTCCTGGAT
37661_at	1255	TAGTTTATCTCAGTCCTGGATGGGA
37661_at	1256	ATCTCAGTCCTGGATGGGAGAGAGA
37661_at	1257	CAAAGAGCCCTGGATCGTTGAATTG
37661_at	1258	CCCTGGATCGTTGAATTGATAGTTT
37661_at	1259	TTGTTCCCTGTTTCATAGATGGGAAGC
37661_at	1260	GTTCCCTGTTTCATAGATGGGAAGCTT
37661_at	1261	AGATGGGAAGCTTCCTTATAACTGA
37661_at	1262	GAAGCTTCCTTATAACTGATGCAGA
37661_at	1263	TCCTTATAACTGATGCAGAGAAAAA
37661_at	1264	CCTTATAACTGATGCAGAGAAAAAT
37661_at	1265	AGTTATGACATCTGTCCTAATTAGT
36393_at	1266	CCTCTCTGTCCCTTGGCAAATGGAC
36393_at	1267	CTGTCCCTTGGCAAATGGACACCAG
36393_at	1268	TCCCTTGGCAAATGGACACCAGGGG
36393_at	1269	GGCAAATGGACACCAGGGGGCTTCTC
36393_at	1270	CAAATGGACACCAGGGGGCTTCTCCC
36393_at	1271	CCAGCCAGGGGCATGGACAGAGCCT
36393_at	1272	CAGCCAGGGGCATGGACAGAGCCTT
36393_at	1273	ATGGACAGAGCCTTTTTCTAAAGAA
36393_at	1274	TGGACAGAGCCTTTTTCTAAAGAAA
36393_at	1275	TGACGGCAGCCGTGCGGACCTACCG
36393_at	1276	AGCCGTGCGGACCTACCGCTGGCAG
36393_at	1277	CGGACCTACCGCTGGCAGTGCATCG
36393_at	1278	ATCGAGTGCAAATCCTGCAGCCTGT
36393_at	1279	CAGCCTGTGCGGAACCTCCGAGAAC
36393_at	1280	AACCTCCGAGAACGACGGTGCCAGC
36393_at	1281	CCTCCGAGAACGACGGTGCCAGCTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39994_at	1282	GGAGGGACTCATCATTTCCATTTAC
39994_at	1283	GAGGGACTCATCATTTCCATTTACC
39994_at	1284	CTCTTCTTTTCAAGTTGGGTGATAT
39994_at	1285	TTATTGCAGCGATTAATAACAGGCA
39994_at	1286	TTTGTTCTTCATCTAAGCCTTCTGG
39994_at	1287	GTTCTTCATCTAAGCCTTCTGGTTT
39994_at	1288	CATCTAAGCCTTCTGGTTTTATGGG
39994_at	1289	CTTCTGGTTTTATGGGTCAGAGTTC
39994_at	1290	TTTTATGGGTCAGAGTTCCGACTGC
39994_at	1291	GTCAGAGTTCCGACTGCCATCTTGG
39994_at	1292	GTTCCGACTGCCATCTTGGACTTGT
39994_at	1293	ACTGCCATCTTGGACTTGTCAGCAA
39994_at	1294	CCATCTTGGACTTGTCAGCAAAAAA
39994_at	1295	CGAGAAGGCCCTTAACTCAAAGTAG
39994_at	1296	GGACCCCTTATTTATCATGCCTTTG
39994_at	1297	AAATGTGCCCACTGTGTGCTTTTGA
35597_at	1298	CCTGGCATTTCATTTCTAAAGATG
35597_at	1299	ACATGGCTGCCCAGCCTACGTGAGC
35597_at	1300	CTACGTGAGCCCTGAGATCCTCAAC
35597_at	1301	CACCACTGGGACCTACTCCGGAAAG
35597_at	1302	CCTACTCCGGAAAGGCTGCGGACGT
35597_at	1303	GGGTGATGCTCTACACCCTTCTGGT
35597_at	1304	TGCTCTACACCCTTCTGGTTGGACG
35597_at	1305	TACACCCTTCTGGTTGGACGATACC
35597_at	1306	CAGTGCCCTTTTCTCCAAAATTCGG
35597_at	1307	AAATTCGGCGTGGACAGTTCTGCAT
35597_at	1308	GACAGTTCTGCATTCCTGAGCACAT
35597_at	1309	GTTCTGCATTCCTGAGCACATTTCC
35597_at	1310	AGACGGGAGCCCTCCGAGAGACTCA
35597_at	1311	CGAGATCCTACTGCACCCCTGGTTT
35597_at	1312	CACCCCTGGTTTGAGTCCGTCTTGG
35597_at	1313	AATAGGAACTTCAGACCAGATTGTT
36780_at	1314	CTACCAGTGGAAGATGCTCAACACC
36780_at	1315	AAGGCGAAGACCAGTACTATCTGCG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36780_at	1316	TCTGCGGGTCACCACGGTGGCTTCC
36780_at	1317	TGAGGTGGTCGTGAAGCTCTTTGAC
36780_at	1318	GGTCGTGAAGCTCTTTGACTCTGAT
36780_at	1319	GAAGCTCTTTGACTCTGATCCCATC
36780_at	1320	CTTTGACTCTGATCCCATCACTGTG
36780_at	1321	AGATGTGGATGTTGCTTTTGCACCT
36780_at	1322	CCAGAGAGAGCTCTGCACGTCACCA
36780_at	1323	AGAGAGCTCTGCACGTCACCAAGTA
36780_at	1324	CTCTGCACGTCACCAAGTAACCAGG
36780_at	1325	GGATCCTGCACTCTAACACTCGACT
36780_at	1326	TGCACTCTAACACTCGACTCTGCTG
36780_at	1327	CTAACACTCGACTCTGCTGCTCATG
36780_at	1328	TAACACTCGACTCTGCTGCTCATGG
36780_at	1329	AACACTCGACTCTGCTGCTCATGGG
34476_r_at	1330	CTGACTTTTGTAAATTCAGTAATG
34476_r_at	1331	TTTAAAAACCTGTATCTGACCCACT
34476_r_at	1332	TCCATTCTGTAGACTTTTGAAAAAA
34476_r_at	1333	AGTTTTTAATTTGATGCCCAATATA
34476_r_at	1334	TATTCTGACCGTTAAAAAATTCTTG
34476_r_at	1335	TTAAAAAATTCTTGTTTCATATGGGA
34476_r_at	1336	TCATATGGGAGAAGGGGGAGTAATG
34476_r_at	1337	GTAATGACTTGTACAAACAGTATTT
34476_r_at	1338	TTGTACAAACAGTATTTCTGGTGTA
34476_r_at	1339	CTTTTATTTTGCACCTCTGTAATTG
34476_r_at	1340	ATTTTGCACCTCTGTAATTGCACTTT
34476_r_at	1341	TTGCACTCTGTAATTGCACTTTTTA
34476_r_at	1342	CACTCTGTAATTGCACTTTTTTAAGT
34476_r_at	1343	AATTGCACTTTTTTAAGTTTGAAGAG
34476_r_at	1344	ATTGCACTTTTTTAAGTTTGAAGAGC
34476_r_at	1345	GTTTGAAGAGCCATTTTGGTAAACG
33862_at	1346	TCACTTGGCGAGGAGCCCGCCTGCT
33862_at	1347	CCTCCTGCAGTTCACCTTGATCATG
33862_at	1348	AGTTCACCTTGATCATGATGGCCTT
33862_at	1349	TCATGATGGCCTTCTACACGGGACT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
33862_at	1350	CCAGTGATGTTCTGGCAGGATTTGC
33862_at	1351	ATGTTCTGGCAGGATTTGCTCAAGG
33862_at	1352	TGGCAGGATTTGCTCAAGGAGCCCT
33862_at	1353	CTCAAGGAGCCCTGGTGGCCTGCTG
33862_at	1354	TGGTGGCCTGCTGCATAGTTTTCTT
33862_at	1355	AAGACTAAGACGACGCTCTCCCTGC
33862_at	1356	CTGCCCCTGCTATCCGGAAGGAAAT
33862_at	1357	CCACAACATGATGTAGGTGCCACCC
33862_at	1358	CACCTCCTGAGCTGTTTTTGTA AAA
33862_at	1359	CAGCAAGTTCTTGCTGCTCTCCAAT
33862_at	1360	AGCAAGTTCTTGCTGCTCTCCAATC
33862_at	1361	AAATGTTTTACTATGTGGCCTTCCA
40769_r_at	1362	CCTGGCCATGAGCCTGTCTCCGACC
40769_r_at	1363	CCATGAGCCTGTCTCCGACCCTGAA
40769_r_at	1364	GAGCCTGTCTCCGACCCTGAAGGGC
40769_r_at	1365	GCCTGTCTCCGACCCTGAAGGGCAG
40769_r_at	1366	CCTGTCTCCGACCCTGAAGGGCAGG
40769_r_at	1367	CTGTCTCCGACCCTGAAGGGCAGGC
40769_r_at	1368	TCCGACCCTGAAGGGCAGGCTGTTG
40769_r_at	1369	CCGACCCTGAAGGGCAGGCTGTTGC
40769_r_at	1370	CGACCCTGAAGGGCAGGCTGTTGCT
40769_r_at	1371	GACCCTGAAGGGCAGGCTGTTGCTG
40769_r_at	1372	AGGGCAGGCTGTTGCTGATGAGGCC
40769_r_at	1373	GGGCAGGCTGTTGCTGATGAGGCCC
40769_r_at	1374	GGCAGGCTGTTGCTGATGAGGCCCA
40769_r_at	1375	AGGCTGTTGCTGATGAGGCCCAAGG
40769_r_at	1376	GGCTGTTGCTGATGAGGCCCAAGGC
40769_r_at	1377	TGTTGCTGATGAGGCCCAAGGCAGG
41790_at	1378	CATAGCTACCGTGAGTTCTCAGCAG
41790_at	1379	AATTAGCCACGTAACAAGAGTCTAT
41790_at	1380	AACTTGAAATTGTGCCACATGACTT
41790_at	1381	AATTACCTGTGTGCAGCTATTTTAA
41790_at	1382	CATTGTTTCATGCTATACTTTGTGG
41790_at	1383	CATGCTATACTTTGTGGGATAAAAC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
41790_at	1384	TTGCTTTTAAAACGTGGACATAACT
41790_at	1385	TGCTTTTAAAACGTGGACATAACTC
41790_at	1386	GCTTTTAAAACGTGGACATAACTCA
41790_at	1387	CGTGGACATAACTCATTITTTCTAGT
41790_at	1388	TTAGTGTCTAGTCTGCAGAGAGCT
41790_at	1389	TTAGTGTCTAGTCTGCAGAGAGCTG
41790_at	1390	AGTGTCTAGTCTGCAGAGAGCTGTG
41790_at	1391	GTGTCTAGTCTGCAGAGAGCTGTGT
41790_at	1392	GTCTAGTCTGCAGAGAGCTGTGTGA
41790_at	1393	TCTAGTCTGCAGAGAGCTGTGTGAT
40456_at	1394	GAGCCATTCAGAAAAGACTTCCTTT
40456_at	1395	AGACTTCCTTTGTGTTTCAGCCTATA
40456_at	1396	GACTTCCTTTGTGTTTCAGCCTATAC
40456_at	1397	TCACACTCCCAAGTCACTTAAGGTG
40456_at	1398	CAAAGCCCAACAATGATCTCAGGAA
40456_at	1399	AAATGTTTTTCATGTAGCAGCAATGC
40456_at	1400	AATGTTTTTCATGTAGCAGCAATGCA
40456_at	1401	TTCATGTAGCAGCAATGCAGATTTG
40456_at	1402	CATGTAGCAGCAATGCAGATTTGGT
40456_at	1403	GTATGTATTTCACTTTATGACTGAC
40456_at	1404	TATTGTTTGGCCAAATAGTAAACAC
40456_at	1405	CACCATGTGTTTGTCTTTGTGAAGGT
40456_at	1406	AGACAAACATAACTATTTAGCAGAG
40456_at	1407	GACAAACATAACTATTTAGCAGAGA
40456_at	1408	CAGCTGGACTGCTGTACATCAAGGA
40456_at	1409	GCTGTACATCAAGGACAGATTAACT
40647_at	1410	TCTTTGGTCTTCTCGACAGGTGCCC
40647_at	1411	GTCTTCTCGACAGGTGCCCTTTCTC
40647_at	1412	CCACTGAATCTGAGAAAGTACTTTC
40647_at	1413	TGGAAACCACCTTAAAACATTAGTG
40647_at	1414	CACCTTAAAACATTAGTGCTATGGT
40647_at	1415	ACCTTAAAACATTAGTGCTATGGTT
40647_at	1416	GTGTATGTGCCAGTACTTACCAGTC
40647_at	1417	ATGTGCCAGTACTTACCAGTCAATG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40647_at	1418	TGCCAGTACTTACCAGTCAATGCAT
40647_at	1419	ACCAGTCAATGCATTGTGGATATGA
40647_at	1420	GGATATGAGCTTTCGTTGACTGCTT
40647_at	1421	TATGAGCTTTCGTTGACTGCTTCTC
40647_at	1422	AGCTTTCGTTGACTGCTTCTCTGCA
40647_at	1423	TTCGTTGACTGCTTCTCTGCAGTCG
40647_at	1424	TTGACTGCTTCTCTGCAGTCGTTGA
40647_at	1425	CTCTGCAGTCGTTGATGCTAATAAA
31834_r_at	1426	TCTGAATAAACTAATACTTAAAATG
31834_r_at	1427	ATCTGTACAGCATTAGATTTTTATA
31834_r_at	1428	CTGTACAGCATTAGATTTTTATATT
31834_r_at	1429	CTGTTTCCCATTTGTCCTCCTACTCA
31834_r_at	1430	TTTCCCATTTGTCCTCCTACTCAACT
31834_r_at	1431	TTCCCATTTGTCCTCCTACTCAACTA
31834_r_at	1432	TCCCATTTGTCCTCCTACTCAACTAA
31834_r_at	1433	CATTGTCCTCCTACTCAACTAAAAT
31834_r_at	1434	GTCCTCCTACTCAACTAAAATTTCAT
31834_r_at	1435	CCTCCTACTCAACTAAAATTTCATAG
31834_r_at	1436	CTACTCAACTAAAATTTCATAGTTGG
31834_r_at	1437	CTCAACTAAAATTTCATAGTTGGCTT
31834_r_at	1438	CAACTAAAATTTCATAGTTGGCTTTA
31834_r_at	1439	TAAAATTTCATAGTTGGCTTTAAGCC
31834_r_at	1440	TAAGCCCCAAAAGAATTTTGAACAAT
31834_r_at	1441	AATTTTGAACAATGTGACAGAAACA
38119_at	1442	ATGCAGCCCTGCAGGGAGACCCTGC
38119_at	1443	TGCCCTCCAAGATGCTGGTGATAGC
38119_at	1444	CCAAGATGCTGGTGATAGCAGCAGA
38119_at	1445	CAAGATGCTGGTGATAGCAGCAGAA
38119_at	1446	GTACTTTATTTGAGGGACAACAGAC
38119_at	1447	GGGACAACAGACTTCACTTCCCTGA
38119_at	1448	GGACAACAGACTTCACTTCCCTGAA
38119_at	1449	CCCTGCTGATACCACCAGACAGAGA
38119_at	1450	ACACTAGGTGCCTGCCCAGGGAGGA
38119_at	1451	GAGGACTCGCGCTACAAGAGGCCAC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38119_at	1452	GGACTCGCGCTACAAGAGGCCACTC
38119_at	1453	CAGAGGCCACCTTTTGCTCCACGGA
38119_at	1454	GGCCACCTTTTGCTCCACGGAGGTG
38119_at	1455	ATAAGTCATCTGTATGCTGACTGGG
38119_at	1456	AGTCATCTGTATGCTGACTGGGGAT
38119_at	1457	ATAATGGCATCAAATGTGTCAGTCCTT
1670_at	1458	AGTCTGGTCCCCAAGGCTCTGGAGC
1670_at	1459	CTGGAGCCATACGTGACAGAAATGG
1670_at	1460	CCATACGTGACAGAAATGGCTCAGG
1670_at	1461	GGAAGTGTGGAGGCGTGTCATCA
1670_at	1462	TCTAACGGCACAAGGTTCTCTGCCA
1670_at	1463	AGGTTCTCTGCCAGTGACCTGACCA
1670_at	1464	TCTGCCAGTGACCTGACCAACGGTG
1670_at	1465	AGTGACCTGACCAACGGTGCAGATG
1670_at	1466	GGGATGCTGGCCACAAGCTCCAATG
1670_at	1467	CTGGCCACAAGCTCCAATGGGTCTC
1670_at	1468	GACGATGACTTCAACGAGAATGACG
1670_at	1469	GACTTCAACGAGAATGACGAGGACG
1670_at	1470	TGGCCTAGTCCCAAGAAGATATTGG
1670_at	1471	ATTAGATATGCACCTCTGATAAGC
1670_at	1472	ATATGCACCTCTGATAAGCAAGGAT
1670_at	1473	TGCTCTGCCGAAGACCTTAAAATGG
1649_at	1474	ATGCTGCGTCAGTTCACAGGGAACC
1649_at	1475	CTGCGTCAGTTCACAGGGAACCCCA
1649_at	1476	TTCACAGGGAACCCCAACATTCCAA
1649_at	1477	AACATTCCAAAACCTCGGCGAATCT
1649_at	1478	AAACCTCGGCGAATCTTGCGCTCGG
1649_at	1479	CCTCGGCGAATCTTGCGCTCGGCCT
1649_at	1480	ATCTTGCGCTCGGCCTGGGGCAGCA
1649_at	1481	TTGCGCTCGGCCTGGGGCAGCAACC
1649_at	1482	TACACACAGGTGGGCTCCAGCGGGG
1649_at	1483	CCCTGCCGTTACACAGAGAGCTCAA
1649_at	1484	CGTTACACAGAGAGCTCAAAGACAG
1649_at	1485	CCCATGCAGGTGCTGTTTTCCGGTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1649_at	1486	ATGCAGGTGCTGTTTTCCGGTGAGG
1649_at	1487	GTGCTGTTTTCCGGTGAGGCCACCC
1649_at	1488	CACGGTGCTCTGCTGTCCGGCCAGC
1649_at	1489	GGTGCTCTGCTGTCCGGCCAGCGTG
38868_at	1490	CGTACCGAGAGATAGGCAGAAGACT
38868_at	1491	GGAATGAGACTGATCCTGAGTTCGT
38868_at	1492	GAGACTGATCCTGAGTTCGTCAATTG
38868_at	1493	ATAGGATAGGGCACTACAGATTCCG
38868_at	1494	TCCGGTACAGTGACACCCTGGAGCT
38868_at	1495	GTAGTGACAGGCTTGTATGGCAAAC
38868_at	1496	GCTTGTATGGCAAACCCTTCCTCTC
38868_at	1497	CCTTCTCTCTGCAGATCGGGGTCT
38868_at	1498	CCTCTCTGCAGATCGGGGTCTGGTG
38868_at	1499	GTTGATGCCAGGAGAGAATATTTCC
38868_at	1500	ATCCCATTTGATAGATTTTCACTGG
38868_at	1501	CTTCTCTTTGGGTCCTGTGGACCTC
38868_at	1502	AACTTGATCCGCATGGCCGTGGCAG
38868_at	1503	TGGCAGGACTGGTCCTCGTGGCTCT
38868_at	1504	ACTGAACAAGGAAGCCTCGGCAGAT
38868_at	1505	CACCAAGTGTCTGCAAGTAAACACC
37952_at	1506	ACATTGGACCTTTCCTGAGGAAGAG
37952_at	1507	AAAGCAGTGGCTCCATTGGTGTTGA
37952_at	1508	CAGTGGCTCCATTGGTGTTGACATA
37952_at	1509	TGGCTCCATTGGTGTTGACATACAT
37952_at	1510	TCTGGCCTCAGTGTTACAGCTAAAT
37952_at	1511	CAGTATCAACATTCTAAGATGCTGG
37952_at	1512	CAACATTCTAAGATGCTGGGACTTA
37952_at	1513	ATGCTGGGACTTACTGTGTCATCAA
37952_at	1514	GGACTTACTGTGTCATCAAATGTGC
37952_at	1515	GAGAGACCTGGCTTTGGCAAGAGCA
37952_at	1516	CCTGGCTTTGGCAAGAGCAGATGTC
37952_at	1517	ACGTCTCTCCTGATGTAGCACTTAA
37952_at	1518	CTCCTGATGTAGCACTTAAGCTTCA
37952_at	1519	ATGTAGCACTTAAGCTTCATTTAGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37952_at	1520	ACACATTTGCATCCACATATTAGGG
37952_at	1521	TTGCATCCACATATTAGGGAAGGAA
654_at	1522	ATCTATTTTGATGCAGCATTTGATA
654_at	1523	ACCTCACTCTTTATAGTGCACAAAA
654_at	1524	TTACCAGCTTTTAACCATCTGATAT
654_at	1525	GCTTTTAACCATCTGATATCTATAG
654_at	1526	GTAGACACACTATCATAGTTAACAT
654_at	1527	AACTATCATAGTTAACATAGTTAA
654_at	1528	TAGTTAAGTTCAGCACTTGTCTCAT
654_at	1529	AGTTCAGCACTTGTCTCATTTTAAT
654_at	1530	TGTAAAGATTTGCTTCCATTTTCCT
654_at	1531	CTTCCATTTTCCTACAGGCAGTCTC
654_at	1532	CACTGTGCAGGTGCTATTGTTACTC
654_at	1533	TTTCTAGCCTGCACTTTGATGTCAT
654_at	1534	GCCTGCACTTTGATGTCATGTGTTT
654_at	1535	ACTTTGATGTCATGTGTTCCCTTTG
654_at	1536	TGTGTTCCCTTTGTCTTTCAAATC
654_at	1537	TCTTGAGACCTTACCCCTGGCTGT
39839_at	1538	AAAGCAAAAAGCAGGCCACAACCTT
39839_at	1539	GGAAGACTAACCAAGATTTGGACAT
39839_at	1540	GAAGACTAACCAAGATTTGGACATT
39839_at	1541	AGACTAACCAAGATTTGGACATTGG
39839_at	1542	GACTAACCAAGATTTGGACATTGGA
39839_at	1543	CTAACCAAGATTTGGACATTGGAAT
39839_at	1544	AGAACCTGGGAATTCCTGCACGGAA
39839_at	1545	AACCTGGGAATTCCTGCACGGAAGA
39839_at	1546	ACCTGGGAATTCCTGCACGGAAGAC
39839_at	1547	GGGAATTCCTGCACGGAAGACAAGA
39839_at	1548	ATTCCTGCACGGAAGACAAGAGAGT
39839_at	1549	TTCCTGCACGGAAGACAAGAGAGTA
39839_at	1550	CCTGCACGGAAGACAAGAGAGTAGC
39839_at	1551	TCTTATGTGACTCTCTTTGAAAATG
39839_at	1552	CTTATGTGACTCTCTTTGAAAATGT
39839_at	1553	TATGTGACTCTCTTTGAAAATGTGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
41743_i_at	1554	ACTGGAAGTGGCAGAGAAGGCTCTG
41743_i_at	1555	AACTGGCAGAGAAGGCTCTGGCTTC
41743_i_at	1556	GCAGAGAAGGCTCTGGCTTCCAAAC
41743_i_at	1557	AAGAGGACCTGGAAACCATGACCAT
41743_i_at	1558	AGATTCACGTGATGGATTGCATCAT
41743_i_at	1559	GATTCACGTGATGGATTGCATCATT
41743_i_at	1560	ATTCACGTGATGGATTGCATCATTT
41743_i_at	1561	TTCACGTGATGGATTGCATCATTTA
41743_i_at	1562	TCACGTGATGGATTGCATCATTTAA
41743_i_at	1563	CATCATTTAAGTGTTGATGTATCAC
41743_i_at	1564	TCCCCAAAAGTGTGGTAAATGTCA
41743_i_at	1565	CCCCAAAAGTGTGGTAAATGTCAG
41743_i_at	1566	CCCCAAAAGTGTGGTAAATGTCAGA
37405_at	1567	AGTCCCAGCCAGAGCCCCTAGTGGT
37405_at	1568	TCACCACGTCGCTGTACAGTGCCTG
37405_at	1569	TCTCATCAGGGAAGGCTCTGTGATG
37405_at	1570	GGCGATTGTAGCTCTGACATCTGGA
37405_at	1571	TCTGACATCTGGATTTGAACTCCAC
37405_at	1572	CTGACATCTGGATTTGAACTCCACC
37405_at	1573	GGCCCTCACTTCCTTGGGGACCTGG
37405_at	1574	CTGGCTTCATTCTGCTCTCTCTTGG
37405_at	1575	GCTTCATTCTGCTCTCTCTTGGCAC
37405_at	1576	TTACTGACCACTGTTGCTTGTGCT
37405_at	1577	TACTGACCACTGTTGCTTGTGCTC
37405_at	1578	CCACTGTTGCTTGTGCTCACTGTG
37405_at	1579	TTGCTTGTGCTCACTGTGCTGCTT
37405_at	1580	CACTGTGCTGCTTTTCCATGAGCTC
37405_at	1581	TTCCATGAGCTCTTGGAGGCACCA
37405_at	1582	CTTGGAGGCACCAAGAAATAAACTC
37323_r_at	1583	CAGTGTAAGCTGCCCTGGATGAGC
37323_r_at	1584	AGTGTAAGCTGCCCTGGATGAGCA
37323_r_at	1585	GTGTAAGCTGCCCTGGATGAGCAG
37323_r_at	1586	TGTAAGCTGCCCTGGATGAGCAGT
37323_r_at	1587	GAGCAGTTTGAACCTCAGAAGACTC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37323_r_at	1588	GGATTCACACGCTCAGCAGCGCCCA
37323_r_at	1589	GATTCACACGCTCAGCAGCGCCAC
37323_r_at	1590	ATTCACACGCTCAGCAGCGCCCACC
37323_r_at	1591	TCACACGCTCAGCAGCGCCCACCAT
37323_r_at	1592	CACACGCTCAGCAGCGCCCACCATT
37323_r_at	1593	ACACGCTCAGCAGCGCCCACCATTG
37323_r_at	1594	CACGCTCAGCAGCGCCCACCATTGA
37323_r_at	1595	ACGCTCAGCAGCGCCCACCATTGAT
37323_r_at	1596	GCTCAGCAGCGCCCACCATTGATTG
37323_r_at	1597	AGCAGCGCCCACCATTGATTGCCAA
37323_r_at	1598	GCAGCGCCCACCATTGATTGCCAAT
33336_at	1599	GGCCACAGACTCAACATGTGTGTGT
33336_at	1600	GGGTTCAGCCCAACATAGAGTAAC
33336_at	1601	GCCCAACATAGAGTAACATTATTTG
33336_at	1602	GTAACATTATTTGTACCTCCCAGGC
33336_at	1603	GGAGCTGCTGGGATCCTCCTTATCT
33336_at	1604	GAGCTGCTGGGATCCTCCTTATCTT
33336_at	1605	CTGCTGGGATCCTCCTTATCTTGAC
33336_at	1606	ATCCTCCTTATCTTGACTGGGATGT
33336_at	1607	TCCTTATCTTGACTGGGATGTCCCT
33336_at	1608	TCTTGACTGGGATGTCCCTGTCTCC
33336_at	1609	TTGACTGGGATGTCCCTGTCTCCCC
33336_at	1610	CCCTTGCTCCTTGAACATGGCCAAG
33336_at	1611	CCTTGCTCCTTGAACATGGCCAAGG
33336_at	1612	CCCCTTGATGCCTGGGAATAGGTTT
33336_at	1613	AGGTTTTGCCAATAAACGTATCTGT
33336_at	1614	GGTTTTGCCAATAAACGTATCTGTG
36229_at	1615	CTCCCGAGGACCTGGAGAGCCTGAG
36229_at	1616	AGCGGCAGCTGCTTTTCCGCCAGCT
36229_at	1617	GGCAGCTGCTTTTCCGCCAGCTGCA
36229_at	1618	TGCTTTTCCGCCAGCTGCAGAAGAA
36229_at	1619	GCCAGCTGCAGAAGAAGCTCGGGCTG
36229_at	1620	AGGGACCGCCCAGATCCCAGCTTTG
36229_at	1621	GGGACCGCCCAGATCCCAGCTTTGA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36229_at	1622	CGCCCAGATCCCAGCTTTGAGAGAG
36229_at	1623	TCCCAGCTTTGAGAGAGGAGTGTGT
36229_at	1624	AGTGTGTGTGCACGTATTCATCTGT
36229_at	1625	ACATGTCTGCATGTGTATATGTTTCG
36229_at	1626	CATGTCTGCATGTGTATATGTTTCGT
36229_at	1627	TCTGGATTTTAATCCCAGGCATCCC
36229_at	1628	TGTGCAGCGGTCTGGTTATCGTCTA
36229_at	1629	GGTTATCGTCTATCCCCAGGGGAAT
36229_at	1630	TCGTCTATCCCCAGGGGAATCCACA
39072_at	1631	GTTAAGTTCAGCACTTGTCTCATTT
39072_at	1632	GTTCAGCACTTGTCTCATTTTAATG
39072_at	1633	GCACTTGTCTCATTTTAATGTAAAG
39072_at	1634	AGATTTGCTTCCATTTTCCTACAGG
39072_at	1635	TTTGCTTCCATTTTCCTACAGGCAG
39072_at	1636	GCTTCCATTTTCCTACAGGCAGTCT
39072_at	1637	AGGCAGTCTCTCTCTTCCTCACAGT
39072_at	1638	CTCACAGTCCCAGTGTGCAGGTGCT
39072_at	1639	TCACAGTCCCAGTGTGCAGGTGCTA
39072_at	1640	GTCCCAGTGTGCAGGTGCTATTGTT
39072_at	1641	CTGTGCAGGTGCTATTGTTACTCTT
39072_at	1642	TGTGCAGGTGCTATTGTTACTCTTA
39072_at	1643	GTGCTATTGTTACTCTTACGAATAT
39072_at	1644	TCTTCTAAGTGAAATTTCTAGCCTG
39072_at	1645	TAAGTGAAATTTCTAGCCTGCACTT
39072_at	1646	CTGCACTTTGATGTCATGTGTTCCC
36790_at	1647	GAGAAGTTCATTCAAAGTGCCAAT
36790_at	1648	AAGTTCATTCAAAGTGCCAATGAT
36790_at	1649	AGTTCATTCAAAGTGCCAATGATA
36790_at	1650	GTTCCATTCAAAGTGCCAATGATAG
36790_at	1651	TTCCATTCAAAGTGCCAATGATAGA
36790_at	1652	ATTCAAAGTGCCAATGATAGAGTCA
36790_at	1653	TTCAAAGTGCCAATGATAGAGTCAA
36790_at	1654	AACACAATCAGGTGTGGATTGGTGCT
36790_at	1655	CACAATCAGGTGTGGATTGGTGCTA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36790_at	1656	ACAATCAGGTGTGGATTGGTGCTAC
36790_at	1657	CAATCAGGTGTGGATTGGTGCTACT
36790_at	1658	TTGGTGCTACTTTGAACAAAAGGTC
36790_at	1659	TGGTGCTACTTTGAACAAAAGGTCC
36790_at	1660	TCCCCCTGTGGTCTTTTGTTCACA
36790_at	1661	CCCCCTGTGGTCTTTTGTTCACAT
36790_at	1662	GGTCTTTTGTTCACATTGTACAAT
41442_at	1663	TCCCCAGGGAAGACCCTGACCGTGT
41442_at	1664	AGGGAAGACCCTGACCGTGTACATA
41442_at	1665	ACCCTGACCGTGTACATAGCCCTGG
41442_at	1666	CCTGACCGTGTACATAGCCCTGGTG
41442_at	1667	CTGACCGTGTACATAGCCCTGGTGC
41442_at	1668	GACCGTGTACATAGCCCTGGTGCTC
41442_at	1669	TGTACATAGCCCTGGTGCTCCTGCC
41442_at	1670	GGTGTGTCTCGGTGACGTTTTCTAT
41442_at	1671	GTGTGTCTCGGTGACGTTTTCTATC
41442_at	1672	CGTTTTCTATCAGACGTGCTCCCTC
41442_at	1673	TCTCAACTGCCTCAGCGATTTCAAG
41442_at	1674	CTCAACTGCCTCAGCGATTTCAAGA
41442_at	1675	AGTACAAGGACAGACAGCAGGCACG
41442_at	1676	CCGCAGCCTGGCATCTGTGCGTGTG
41442_at	1677	GCCTGGCATCTGTGTGCGTGGCTAT
41442_at	1678	ATGTATATAGTCTTTGCAGAGGTCC
1519_at	1679	GAGGACCCAGGAAAGGCAGGATTGA
1519_at	1680	GCCAAGAAGCAGTGGCCTTATTGCA
1519_at	1681	AAGCAGTGGCCTTATTGCATCCCAA
1519_at	1682	TGGCCTTATTGCATCCCAAACCACG
1519_at	1683	TATTGCATCCCAAACCACGCCTCTT
1519_at	1684	GGCTGCCTCCCTTGTGGCAGCAACG
1519_at	1685	AGCAACGGCACAGCTAATTCTACTC
1519_at	1686	GGCACAGCTAATTCTACTCACAGTG
1519_at	1687	GCTAATTCTACTCACAGTGCTTTTA
1519_at	1688	ATGGTTCTGGCTGTTTGAGATTCTC
1519_at	1689	GTTTGAGATTCTCAAAGGAGCGAGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1519_at	1690	GATTCTCAAAGGAGCGAGCATGTTCG
1519_at	1691	CAAAGGAGCGAGCATGTCTGTGGACA
1519_at	1692	AGCGAGCATGTCTGTGGACACACACA
1519_at	1693	GTGGACACACACAGACTATTTTTAG
1519_at	1694	GAAACAACCATGTCATTTTCAGAAGT
33080_s_at	1695	TGTCAGGGGGACCTGGGCATTCTCT
33080_s_at	1696	GGACCTGGGCATTCTCTGGGGCCCT
33080_s_at	1697	GACCTGGGCATTCTCTGGGGCCCTC
33080_s_at	1698	TCTCTGGGGCCCTCCTTTGACATAT
33080_s_at	1699	CTCTGGGGCCCTCCTTTGACATATA
33080_s_at	1700	TCTGGGGCCCTCCTTTGACATATAC
33080_s_at	1701	CTGGGGCCCTCCTTTGACATATACC
33080_s_at	1702	TGGGGCCCTCCTTTGACATATACCC
33080_s_at	1703	GGGGCCCTCCTTTGACATATACCCA
33080_s_at	1704	GGGCCCTCCTTTGACATATACCCAG
33080_s_at	1705	CCTCCTTTGACATATACCCAGCGAG
33080_s_at	1706	CTCCTTTGACATATACCCAGCGAGC
33080_s_at	1707	TCCTTTGACATATACCCAGCGAGCA
33080_s_at	1708	CCTTTGACATATACCCAGCGAGCAC
33080_s_at	1709	TGACATATACCCAGCGAGCACTTTG
33080_s_at	1710	CGGATCATGGTGATAGGAGGAACCC
34742_at	1711	TTCCTGACGGGCATGACTGTGGCCG
34742_at	1712	CGGAAATGACCAGACACTGACCATC
34742_at	1713	GAAATGACCAGACACTGACCATCCA
34742_at	1714	GCCATTGCCACCAGGAGAACCACTA
34742_at	1715	GAGAACCACTACATGCAGCCCATGC
34742_at	1716	GGTTGGGCCCCAGATCTGGTCCCTTG
34742_at	1717	GCAGCTAGTTTTCTAGAATTTATCA
34742_at	1718	CTAGAATTTATCACACTTCTGTGAG
34742_at	1719	GAATTTATCACACTTCTGTGAGACC
34742_at	1720	ACCTCAGTTCCCTTGGCCTCAGAAT
34742_at	1721	GTTCCCTTGGCCTCAGAATTCACAA
34742_at	1722	TTCCACAAAATCTGTCCAAAGGAG
34742_at	1723	TCTGTCCAAAGGAGGCTGGCAGGTA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34742_at	1724	ATGTTTGTGGCCTCAGAATTGATCA
34742_at	1725	TGGCCTCAGAATTGATCATTTTCCC
34742_at	1726	CACTTGTTCCAGCTCTTTGAAATAG
37026_at	1727	CCTGCACATGAAGAGGCACCTCTGA
37026_at	1728	ATGAAGAGGCACCTCTGAGGGAGCA
37026_at	1729	CTCCAGGGCCTCTCCTTGGAAGGTC
37026_at	1730	TCCAGGGCCTCTCCTTGGAAGGTCT
37026_at	1731	GCCTCTCCTTGGAAGGTCTTTTGAG
37026_at	1732	ATGGTATGTGGGTGACCCTGGACTC
37026_at	1733	GGTGACCCTGGACTCGCCACTGGTA
37026_at	1734	CGAGCGGCGCCTAAGCCTTTGCCGT
37026_at	1735	CACACTGAGAATGCTAATGGTTGGG
37026_at	1736	TGTTGAGGATCTATTACTGACCGTA
37026_at	1737	TGACCGTATGATGAGGCCAACTTTT
37026_at	1738	AGTATACCATGAGATGAGATGACCA
37026_at	1739	GTATACCATGAGATGAGATGACCAC
37026_at	1740	TATACCATGAGATGAGATGACCACC
37026_at	1741	AGATGAGATGACCACCAATCATTTT
37026_at	1742	AGCCTTTTAAATGCTCCCCTGTGA
34777_at	1743	TGCCAGGCTTAAGGAGAGGAGAAAC
34777_at	1744	CGTGCTCGCCCACAACTGATTTCT
34777_at	1745	CAAACCTGATTTCTCACGGCGTGTCA
34777_at	1746	GCGCAAGCCTCACTATTACTTGAAC
34777_at	1747	AAGTGCAATGCGTGTTGTACATACA
34777_at	1748	TGCAATGCGTGTTGTACATACAGAG
34777_at	1749	TGTACATACAGAGGTAACCTATCAAT
34777_at	1750	CCCCTATTTTAAGACGTGAATGTCT
34777_at	1751	GACGTGAATGTCTCAGCGAGGTGTA
34777_at	1752	GTGTAAAGTTGTTTCGCCGCGTGGAA
34777_at	1753	GAAAGACTGATTACCTCCTGTGTGG
34777_at	1754	CTGATTACCTCCTGTGTGGAAGAAG
34777_at	1755	ACCTCCTGTGTGGAAGAAGGAAACA
34777_at	1756	GAAACACCGAGTCTCTGTATAATCT
34777_at	1757	ATGCGAACAGCAAACCAATAAACTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34777_at	1758	TCCTTAGCCTTGCTCAGGTGCAAGT
36037_g_at	1759	GAGGCTCCAGTTTCCCACCATGCGG
36037_g_at	1760	CACCATGCGGCCACCGAGAGAACGT
36037_g_at	1761	CACCGAGAGAACGTCCCCGGTCAGT
36037_g_at	1762	GAACGTCCCCGGTCAGTCTCTGGTC
36037_g_at	1763	AACGTCCCCGGTCAGTCTCTGGTCT
36037_g_at	1764	GTCCCCGGTCAGTCTCTGGTCTCGT
36037_g_at	1765	GTCAGTCTCTGGTCTCGTTTGTCTA
36037_g_at	1766	CTGGTCTCGTTTGTCTAGTTCCTGG
36037_g_at	1767	GTCTCGTTTGTCTAGTTCCTGGGAG
36037_g_at	1768	TCGTTTGTCTAGTTCCTGGGAGTCA
36037_g_at	1769	TTGTCTAGTTCCTGGGAGTCACTGC
36037_g_at	1770	CTAGTTCCTGGGAGTCACTGCAGCC
36037_g_at	1771	TAGTTCCTGGGAGTCACTGCAGCCA
36037_g_at	1772	AGTTCCTGGGAGTCACTGCAGCCAG
36037_g_at	1773	TGGGAGTCACTGCAGCCAGAGCCCT
36037_g_at	1774	GGGAGTCACTGCAGCCAGAGCCCTC
40644_g_at	1775	CGAGGCTTCAGGATCCAGTTCTCGT
40644_g_at	1776	GGCTTCAGGATCCAGTTCTCGTAAG
40644_g_at	1777	CTTCAGGATCCAGTTCTCGTAAGCT
40644_g_at	1778	AGGATCCAGTTCTCGTAAGCTGCGA
40644_g_at	1779	TCCAGTTCTCGTAAGCTGCGACTCG
40644_g_at	1780	AGTTCTCGTAAGCTGCGACTCGGCG
40644_g_at	1781	GTTCTCGTAAGCTGCGACTCGGCGC
40644_g_at	1782	TCGTAAGCTGCGACTCGGCGCCCTG
40644_g_at	1783	GTAAGCTGCGACTCGGCGCCCTGTA
40644_g_at	1784	GACTCGGCGCCCTGTACTGTGGTGC
40644_g_at	1785	TCGGCGCCCTGTACTGTGGTGCAGT
40644_g_at	1786	CGCCCTGTACTGTGGTGCAGTGTGA
40644_g_at	1787	TGTACTGTGGTGCAGTGTGACCTGC
40644_g_at	1788	GTACTGTGGTGCAGTGTGACCTGCA
40644_g_at	1789	CCATGGTCACGGTGCTGGCCTTCCT
40644_g_at	1790	ATGGTCACGGTGCTGGCCTTCCTGT
35331_at	1791	TCTATGCCACCAGCTCCAGACAGTA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35331_at	1792	TATGCCACCAGCTCCAGACAGTAAC
35331_at	1793	TGCCACCAGCTCCAGACAGTAACTA
35331_at	1794	CCACCAGCTCCAGACAGTAACTAAG
35331_at	1795	CACCAGCTCCAGACAGTAACTAAGA
35331_at	1796	ACCAGCTCCAGACAGTAACTAAGAC
35331_at	1797	CAGCTCCAGACAGTAACTAAGACTT
35331_at	1798	AGCTCCAGACAGTAACTAAGACTTC
35331_at	1799	GCTCCAGACAGTAACTAAGACTTCT
35331_at	1800	AACGGATGGGTCTCAGTTACAAATA
35331_at	1801	ATGGGTCTCAGTTACAAATAAGGAC
35331_at	1802	GTCTCAGTTACAAATAAGGACACTA
35331_at	1803	CTTTTGGGGTCAGATCTCTGGAACA
35331_at	1804	TTGGGGTCAGATCTCTGGAACATCA
35331_at	1805	ACATCATGTGATGAAGCTGACATTT
35331_at	1806	GCTCTATTTTCTGATCATGAAACTG
875_g_at	1807	TGGGTTTCAGGATTCCATGGACCACC
875_g_at	1808	AGGATTCCATGGACCACCTGGACAA
875_g_at	1809	TTCCATGGACCACCTGGACAAGCAA
875_g_at	1810	ACTCCGAAGACTTGAACACTCACTC
875_g_at	1811	CGAAGACTTGAACACTCACTCCACA
875_g_at	1812	TTGAACACTCACTCCACAACCCAAG
875_g_at	1813	CACAACCCAAGAATCTGCAGCTAAC
875_g_at	1814	ACCCAAGAATCTGCAGCTAACTTAT
875_g_at	1815	AACATTATGCCTTAAGTAATGTAA
875_g_at	1816	AGTTTATCTTTCATGGTACTAGTGT
875_g_at	1817	GAAATTGCTTTTCTCTTGAACCAC
875_g_at	1818	TTTCTCTTGAACCACAGTTCTACC
875_g_at	1819	TTGAACCACAGTTCTACCCCTGGGA
875_g_at	1820	CAGTTCTACCCCTGGGATGTTTTGA
875_g_at	1821	TACCCCTGGGATGTTTTGAGGGTCT
875_g_at	1822	TGTTTTGAGGGTCTTTGCAAGAATC
35773_i_at	1823	TTCCCCGAACGCAAGGAGCGCGAGA
35773_i_at	1824	TCCCCGAACGCAAGGAGCGCGAGAT
35773_i_at	1825	CCCCGAACGCAAGGAGCGCGAGATG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35773_i_at	1826	AGCGCGAGATGGTGGCCACACAGCA
35773_i_at	1827	AGATGGTGGCCACACAGCAGGAGAT
35773_i_at	1828	ACACAGCAGGAGATGATGGACGCGC
35773_i_at	1829	TGAGGCTCCAGCTGCGGGACTACTG
35773_i_at	1830	TAGGAGCTAGGTGACCCTCGGCTGC
35773_i_at	1831	AGGAGCTAGGTGACCCTCGGCTGCT
35773_i_at	1832	GCTAGGTGACCCTCGGCTGCTGCAG
35773_i_at	1833	AGTGGACCCCAAGGTGGCCCTGTAG
35773_i_at	1834	GTGACCCTCGGCTGCTGCAGGGATC
35773_i_at	1835	TGACCCTCGGCTGCTGCAGGGATCT
39802_at	1836	TCAATAAGAAAATCCCTAAGCAGAG
39802_at	1837	AAGCAGAGGCTGGAGAGCTACAGAA
39802_at	1838	AGCTACAGAAGGACCACCAGTAGCC
39802_at	1839	GCTACAGAAGGACCACCAGTAGCCA
39802_at	1840	TACAGAAGGACCACCAGTAGCCACT
39802_at	1841	ACAGAAGGACCACCAGTAGCCACTG
39802_at	1842	CAGAAGGACCACCAGTAGCCACTGT
39802_at	1843	AGAAGGACCACCAGTAGCCACTGTC
39802_at	1844	ACCAGTAGCCACTGTCCCCGGGAAG
39802_at	1845	CAGTAGCCACTGTCCCCGGGAAGCT
39802_at	1846	CCAAAGCTTTGAACATTCATGACTG
39802_at	1847	CAAAGCTTTGAACATTCATGACTGA
39802_at	1848	AGCTTTGAACATTCATGACTGAACT
39802_at	1849	TCCCTTCTCTACCTCATGGGGGTAT
39802_at	1850	CTTGCAAGAATCAGTGCAAAGATTT
39802_at	1851	TAAGATATGATGTCCCTATGGAAGC
37220_at	1852	TTAGTGAACACTGTTCTCTGGGTG
37220_at	1853	TCTCTGGGTGACAATACGTAAAGAA
37220_at	1854	GAAATCTCTTTGGATTCTGGTCATG
37220_at	1855	CTCTTTGGATTCTGGTCATGAGAAG
37220_at	1856	AATTTCCAGCCTTCAAGAAGACAGA
37220_at	1857	CAGCCTTCAAGAAGACAGACATTTA
37220_at	1858	CCTTCAAGAAGACAGACATTTAGAA
37220_at	1859	TGGGTGGCCATCGATCTGGACCGTC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37220_at	1860	GGGTGGCCATCGATCTGGACCGTCC
37220_at	1861	TGCTCCCCGTGAGCACTGCGTACAA
37220_at	1862	ACCAGAACTGTGTGTCTCATGGTAT
37220_at	1863	TGAAATGAGGCCTACTCTAAAGAAT
37220_at	1864	ACTAACTGCTAGAAGAGAAGACTCT
37220_at	1865	AGACTCTGGGTTATACTGGTGCGAG
37220_at	1866	GCGCAGCCCTGAGTTGGAGCTTCAA
37220_at	1867	CCCTGAGTTGGAGCTTCAAGTGCTT
37192_at	1868	AAATGGGAATTCCAGCACTAAGCCA
37192_at	1869	ACCGGGCAGAAGCTGGGCCTTCCGC
37192_at	1870	CAGCTTGACTTCTTTCCAGTCCACG
37192_at	1871	AGCTTGACTTCTTTCCAGTCCACGT
37192_at	1872	GTCCACGTGTGTATATAATGATATC
37192_at	1873	ATATTTTGGCCAGGTCTGGGTATT
37192_at	1874	TTTTGCCCAGGTCTGGGTATTGCTC
37192_at	1875	TTTGCCCAGGTCTGGGTATTGCTCC
37192_at	1876	CCCAGGTCTGGGTATTGCTCCTGCC
37192_at	1877	TCTGGGTATTGCTCCTGCCCAGACC
37192_at	1878	GGGTATTGCTCCTGCCCAGACCCTG
37192_at	1879	CCTGACATCCCTTTCCACTGTGTGT
37192_at	1880	GACATCCCTTTCCACTGTGTGTGTG
37192_at	1881	ACATCCCTTTCCACTGTGTGTGTGA
37192_at	1882	CCACTGTGTGTGTGACCATGCTGGG
37192_at	1883	ACTCTGCTTGGAATTAAGGTTGC
31610_at	1884	GCCTTATCGCGGTGGCCGTGTTCT
31610_at	1885	GTGTTCTGGTCCTCGTTGCAATCG
31610_at	1886	GCCTTTGCAGTCAACCACTTCTGGT
31610_at	1887	GCAGTCAACCACTTCTGGTGCCAGG
31610_at	1888	AACCACTTCTGGTGCCAGGAGGAGC
31610_at	1889	AGGAGGAGCCGGAGCCTGCACACAT
31610_at	1890	GGAAGGTACTCTTCGATGGCGGCCA
31610_at	1891	AAGGTACTCTTCGATGGCGGCCAGT
31610_at	1892	TCGATGGCGGCCAGTTTCAGGTCCA
31610_at	1893	GCGGCCAGTTTCAGGTCCAGTGAGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31610_at	1894	AGGTCCAGTGAGCATGAGAATGCCT
31610_at	1895	GTCCAGTGAGCATGAGAATGCCTAT
31610_at	1896	AGAATGCCTATGAGAATGTGCCCCGA
31610_at	1897	TTCTGGGCCTGCTCACGGCAGTGCC
31610_at	1898	GGCAGTGCCACCTGCCAGCTGTCAG
31610_at	1899	AGCCCTGGATGCAGGGCCTTATCGC
37104_at	1900	TTCTAAAGAGCCTGCGAAAGCCTTT
37104_at	1901	TACAAGGACTTGTACTAGCAGAGAG
37104_at	1902	CAAGGACTTGTACTAGCAGAGAGTC
37104_at	1903	GACTTGTACTAGCAGAGAGTCCTGA
37104_at	1904	CTTGTACTAGCAGAGAGTCCTGAGC
37104_at	1905	TGTACTAGCAGAGAGTCCTGAGCCA
37104_at	1906	TACTAGCAGAGAGTCCTGAGCCACT
37104_at	1907	CTAGCAGAGAGTCCTGAGCCACTGC
37104_at	1908	AGCAGAGAGTCCTGAGCCACTGCCA
37104_at	1909	CAGAGAGTCCTGAGCCACTGCCAAC
37104_at	1910	GAGTCCTGAGCCACTGCCAACATTT
37104_at	1911	TTCTTCCAGTTGCACTATTCTGAGG
37104_at	1912	AGTTGCACTATTCTGAGGGAAAATC
37104_at	1913	GTTGCACTATTCTGAGGGAAAATCT
37104_at	1914	TTGCACTATTCTGAGGGAAAATCTG
37104_at	1915	TGCACTATTCTGAGGGAAAATCTGA
38582_at	1916	TTCTCAGTGCCCTGGCCCTGTTGAG
38582_at	1917	GTGCCTTGGCCCTGTTGAGTCTATC
38582_at	1918	TCTGGTAACACTGGAGCTGACTCCC
38582_at	1919	ACTGGAGCTGACTCCCTGGGAAGAG
38582_at	1920	TGACTCCCTGGGAAGAGAGGCCAAA
38582_at	1921	CTCCCTGGGAAGAGAGGCCAAATGT
38582_at	1922	AATACTTATCCCAATGAATGCGTGT
38582_at	1923	TATCCCAATGAATGCGTGTTATGTT
38582_at	1924	TCCTCATTCAAAAATCTGGGCCTTG
38582_at	1925	CATTCAAAAATCTGGGCCTTGCTGA
38582_at	1926	AATCTGGGCCTTGCTGAGAACCAAG
38582_at	1927	TGCTGAGAACCAAGGTTTTGAAATC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38582_at	1928	TTTTGAAATCCCATCAGGTCACCGC
38582_at	1929	TTGAAATCCCATCAGGTCACCGCGA
38582_at	1930	GCCTGACTGGCCTTATTGTTGAATA
38582_at	1931	CCTGACTGGCCTTATTGTTGAATAA
41169_at	1932	TAAATGCCATGTGGAGATAGAGCCC
41169_at	1933	AAATGCCATGTGGAGATAGAGCCCC
41169_at	1934	ATGCCATGTGGAGATAGAGCCCCAG
41169_at	1935	AGATAGAGCCCCAGATGTTTCAGCC
41169_at	1936	GATAGAGCCCCAGATGTTTCAGCCA
41169_at	1937	ATAGAGCCCCAGATGTTTCAGCCAT
41169_at	1938	TAGAGCCCCAGATGTTTCAGCCATC
41169_at	1939	AGCCCCAGATGTTTCAGCCATCTCA
41169_at	1940	GCCCCAGATGTTTCAGCCATCTCAG
41169_at	1941	GATGTTTCAGCCATCTCAGCCCAGG
41169_at	1942	TGTTTCAGCCATCTCAGCCCAGGCA
41169_at	1943	ATGTAGCCCCAGCAGATGTGATATA
41169_at	1944	TGTAGCCCCAGCAGATGTGATATAG
41169_at	1945	GTAGCCCCAGCAGATGTGATATAGA
41169_at	1946	TAGCCCCAGCAGATGTGATATAGAG
41169_at	1947	CCCCAGCAGATGTGATATAGAGAAG
1274_s_at	1948	CACGCTGGCCGAGTACTGCGTGAAG
1274_s_at	1949	GCTGGCCGAGTACTGCGTGAAGACC
1274_s_at	1950	GCGCCCGACGAGGGCTCAGACCTCT
1274_s_at	1951	CCCGACGAGGGCTCAGACCTCTTCT
1274_s_at	1952	CGACGAGGGCTCAGACCTCTTCTAC
1274_s_at	1953	CGAGGGCTCAGACCTCTTCTACGAC
1274_s_at	1954	GGGCTCAGACCTCTTCTACGACGAC
1274_s_at	1955	ACCTCTTCTACGACGACTACTACGA
1274_s_at	1956	TCTTCTACGACGACTACTACGAGGA
1274_s_at	1957	TCTACGACGACTACTACGAGGACGG
1274_s_at	1958	ACTACTACGAGGACGGCGAGGTGGA
1274_s_at	1959	GCCGACAGCTGCTTCGGGGACGATG
1274_s_at	1960	CTGCTTCGGGGACGATGAGGATGAC
1274_s_at	1961	TTCGGGGACGATGAGGATGACTCTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1274_s_at	1962	ATGACTCTGGCACGGAGGAGTCCTG
1274_s_at	1963	ACTCTGGCACGGAGGAGTCCTGACA
40177_at	1964	ATATTATACTTTAGGGCAACCCTAG
40177_at	1965	TACTTTAGGGCAACCCTAGTTGGCA
40177_at	1966	TTAGGGCAACCCTAGTTGGCAGCTT
40177_at	1967	TAGGGCAACCCTAGTTGGCAGCTTT
40177_at	1968	AGGGCAACCCTAGTTGGCAGCTTTG
40177_at	1969	GGCAACCCTAGTTGGCAGCTTTGAG
40177_at	1970	ACCCTAGTTGGCAGCTTTGAGAGAA
40177_at	1971	CCCTAGTTGGCAGCTTTGAGAGAAG
40177_at	1972	CCTAGTTGGCAGCTTTGAGAGAAGT
40177_at	1973	TTGGCAGCTTTGAGAGAAGTTCTTC
40177_at	1974	TTCCATTAAACATGGAAGGAATAAC
40177_at	1975	AATAGGGAACTTGACAGCAGACAGA
40177_at	1976	ATAGGGAACTTGACAGCAGACAGAG
40177_at	1977	GGAACCTTGACAGCAGACAGAGGGAA
40177_at	1978	GAACTTGACAGCAGACAGAGGGGAAG
40177_at	1979	ACTTGACAGCAGACAGAGGGGAAGAG
35659_at	1980	AGTATCAGACACAGCCCCAGAAGGG
35659_at	1981	TCCCCATAGGCCATTTGGACTCTGC
35659_at	1982	ATAGGCCATTTGGACTCTGCCTTCA
35659_at	1983	GACTCTGCCTTCAAACAAAGGCAGT
35659_at	1984	AGTCCACAGGCATGGAAGCTGTGAG
35659_at	1985	GGGACAGGCCTGTGCGTGCCATCCA
35659_at	1986	CCTGTGCGTGCCATCCAGAGTCATC
35659_at	1987	GCGTGCCATCCAGAGTCATCTCAGC
35659_at	1988	TCAGCCCTGCCTTTCTCTGGAGCAT
35659_at	1989	CCTGCCTTTCTCTGGAGCATTCTGA
35659_at	1990	TGGCCCAGGGAATCCAGCCATGACC
35659_at	1991	ACCCCTCTGCCAAAGTACTCTTAGG
35659_at	1992	TGCCAGTCTGGTAACTGAACTCCCT
35659_at	1993	AACTCCCTCTGGAGGCAGGCTTGAG
35659_at	1994	GGGAGGATTCCCTCAGGGTTCCTTG
35659_at	1995	GGAGGATTCCCTCAGGGTTCCTTGA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35337_at	1996	TCATTCCTGGTCCTGGGGAGACGCC
35337_at	1997	CATTCCTGGTCCTGGGGAGACGCC
35337_at	1998	GACAGATTTCCCTTTAGACCCAGCA
35337_at	1999	ATTTCAATTTCTGGAGCTCCATTTGT
35337_at	2000	TAAACTACAGATGTCAACTCCTTGG
35337_at	2001	ACTACAGATGTCAACTCCTTGGGGT
35337_at	2002	GATGTCAACTCCTTGGGGTGCTGAT
35337_at	2003	AACTCCTTGGGGTGCTGATCTCGAG
35337_at	2004	TGCTGATCTCGAGTGTTATTTTCTG
35337_at	2005	TGCACTCCCAGAAACCTTTTAAGAG
35337_at	2006	GCACTCCCAGAAACCTTTTAAGAGA
35337_at	2007	TTGGCCTTGGGAATAGTTGGCTGCC
35337_at	2008	TAGTTGGCTGCCAATCTCCCTGCTC
35337_at	2009	CCCTGCTCTTGGTTCTCCTCTAGAT
35337_at	2010	TCTTGGTTCTCCTCTAGATTGAAGT
35337_at	2011	TTCTGATGCTGTTCTTACCAGATTA
38584_at	2012	TATTTTCCTGTCAGCATCTGAGCTT
38584_at	2013	CAGCATCTGAGCTTGAGGATGGTAG
38584_at	2014	GGCCAGGGCGCAGTCAGCTCCAGTC
38584_at	2015	CGCAGTCAGCTCCAGTCCCAGAGAG
38584_at	2016	AGTCAGCTCCAGTCCCAGAGAGCTC
38584_at	2017	CCAGAGAGCTCCTCTCTAACTCAGA
38584_at	2018	GCTCCTCTCTAACTCAGAGCAACTG
38584_at	2019	CTCTAACTCAGAGCAACTGAACTGA
38584_at	2020	CTCAGAGCAACTGAACTGAGACAGA
38584_at	2021	CTGAACTGAGACAGAGGAGGAAAAC
38584_at	2022	AACAGAGCATCAGAAGCCTGCAGTG
38584_at	2023	ATCAGAAGCCTGCAGTGGTGGTTGT
38584_at	2024	CCCAACCTGGGATTGCTGAGCAGGG
38584_at	2025	CAGGGAAGCTTTGCATGTTGCTCTA
38584_at	2026	AGCTTTGCATGTTGCTCTAAGGTAC
38584_at	2027	GCATGTTGCTCTAAGGTACATTTTT
1997_s_at	2028	TGGGACGGCCTCCTCTCCTACTTTG
1997_s_at	2029	TCTCCTACTTTGGGACGCCCACTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1997_s_at	2030	TCCTACTTTGGGACGCCCCACGTGGC
1997_s_at	2031	TTGGGACGCCCCACGTGGCAGACCGT
1997_s_at	2032	GGGACGCCCCACGTGGCAGACCGTGA
1997_s_at	2033	GACGCCCCACGTGGCAGACCGTGACC
1997_s_at	2034	CGCCCCACGTGGCAGACCGTGACCAT
1997_s_at	2035	CCCACGTGGCAGACCGTGACCATCT
1997_s_at	2036	CCACGTGGCAGACCGTGACCATCTT
1997_s_at	2037	CACGTGGCAGACCGTGACCATCTTT
1997_s_at	2038	ACGTGGCAGACCGTGACCATCTTTG
1997_s_at	2039	CGTGGCAGACCGTGACCATCTTTGT
1997_s_at	2040	TGGCAGACCGTGACCATCTTTGTGG
1997_s_at	2041	GGCAGACCGTGACCATCTTTGTGGC
1997_s_at	2042	GCAGACCGTGACCATCTTTGTGGCG
1997_s_at	2043	CAGACCGTGACCATCTTTGTGGCGG
36162_at	2044	TGAAGTGTTTCACGAGAGCCCGGGA
36162_at	2045	AGTGTTTCACGAGAGCCCGGGAGCT
36162_at	2046	AGCCTTCTCCACTGGCCGGAGTCAG
36162_at	2047	GTCAGTGCCAGGTCCTTGCCCTTTG
36162_at	2048	CCCTTTGTGGAAAGTCACAGGTCAC
36162_at	2049	GTCTGAAGCCAATGCTGTCTGGTTG
36162_at	2050	ATGCTGTCTGGTTGCGCCATTTTTG
36162_at	2051	TTTATGAGGGCCACGGGTCTGTGTT
36162_at	2052	GGCCACGGGTCTGTGTTGCGACTCAG
36162_at	2053	GCCTCAGGGACGACTCTGACCTCTT
36162_at	2054	ACCTCTTGGCCACAGAGGACTCACT
36162_at	2055	TTGGCCACAGAGGACTCACTTGCCC
36162_at	2056	CCCTCCTTGTCTGTGCATCCGGGGG
36162_at	2057	CGGGACTCCAGAACCGCAGAAGCCT
36162_at	2058	AGGACGGCCGGCTCTCTATAGCACC
36162_at	2059	CTCTCTATAGCACCAGGGCTCACGT
867_s_at	2060	CGAGCTGTGGCAATGGAATTCAGCA
867_s_at	2061	CCTGCGATAGCCTCAACAACCGATG
867_s_at	2062	GCGATAGCCTCAACAACCGATGTGA
867_s_at	2063	TAGCCTCAACAACCGATGTGAGGGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
867_s_at	2064	TGTTGGCCCAGCGACTCTGCGGACG
867_s_at	2065	GGCCCAGCGACTCTGCGGACGATGG
867_s_at	2066	CGACTCTGCGGACGATGGCTGGTCT
867_s_at	2067	CTCTGCGGACGATGGCTGGTCTCCA
867_s_at	2068	CGGACGATGGCTGGTCTCCATGGTC
867_s_at	2069	TCCATGGTCCGAGTGGACCTCCTGT
867_s_at	2070	TGGTCCGAGTGGACCTCCTGTTCTA
867_s_at	2071	TCCGAGTGGACCTCCTGTTCTACGA
867_s_at	2072	AGTGGACCTCCTGTTCTACGAGCTG
867_s_at	2073	GACCTCCTGTTCTACGAGCTGTGGC
867_s_at	2074	CTCCTGTTCTACGAGCTGTGGCAAT
867_s_at	2075	TGTTCTACGAGCTGTGGCAATGGAA
38799_at	2076	CAGGAGGTGCCCTGGTACACCTGCT
38799_at	2077	AGGAGGTGCCCTGGTACACCTGCTT
38799_at	2078	GGAGGTGCCCTGGTACACCTGCTTG
38799_at	2079	GAGGTGCCCTGGTACACCTGCTTGA
38799_at	2080	AGGTGCCCTGGTACACCTGCTTGAC
38799_at	2081	GGTGCCCTGGTACACCTGCTTGACC
38799_at	2082	GTGCCCTGGTACACCTGCTTGACCT
38799_at	2083	TGCCCTGGTACACCTGCTTGACCTT
38799_at	2084	TGGTACACCTGCTTGACCTTCCCTG
38799_at	2085	GGTACACCTGCTTGACCTTCCCTGT
38799_at	2086	GTACACCTGCTTGACCTTCCCTGTG
38799_at	2087	CCATCCCAGATCTCAAAGTGTTTGA
38799_at	2088	CATCCCAGATCTCAAAGTGTTTGAG
38799_at	2089	ATCCCAGATCTCAAAGTGTTTGAGC
38799_at	2090	TCCCAGATCTCAAAGTGTTTGAGCG
38799_at	2091	CCCAGATCTCAAAGTGTTTGAGCGT
34375_at	2092	CCAGATGCAATCAATGCCCCAGTCA
34375_at	2093	AGATGCAATCAATGCCCCAGTCACC
34375_at	2094	AACTTCACCAATAGGAAGATCTCAG
34375_at	2095	ACTTCACCAATAGGAAGATCTCAGT
34375_at	2096	CAGTGCAGAGGCTCGCGAGCTATAG
34375_at	2097	TATAGAAGAATCACCAGCAGCAAGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34375_at	2098	CAAGTGTCCCAAAGAAGCTGTGATC
34375_at	2099	AGCAAACCCAAACTCCGAAGACTTG
34375_at	2100	GCAAACCCAAACTCCGAAGACTTGA
34375_at	2101	GGAAATTGCTTTTCCTCTTGAACCA
34375_at	2102	TCTTGAACCACAGTTCTACCCCTGG
34375_at	2103	GAACCACAGTTCTACCCCTGGGATG
34375_at	2104	CAGTTCTACCCCTGGGATGTTTTGA
34375_at	2105	TACCCCTGGGATGTTTTGAGGGTCT
34375_at	2106	CCCTGGGATGTTTTGAGGGTCTTTG
34375_at	2107	GGTCTTTGCAAGAATCATTAATACA
36628_at	2108	CTCTGTCAGAGTGAACAGCACCGCG
36628_at	2109	CCCACACACACTCAAGGGGGTCGAAA
36628_at	2110	CACACACACTCAAGGGGGTCGAAAAC
36628_at	2111	CTGTCGGTCTCAGTACGTTCACTTT
36628_at	2112	TCAGTACGTTCACTTTATAGCTGCT
36628_at	2113	CTTTATAGCTGCTGGCAATATCGAA
36628_at	2114	AGCTGCTGGCAATATCGAAGGTTCC
36628_at	2115	GGCAATATCGAAGGTTCTTTTTTG
36628_at	2116	GTGTAAACTCTAATTTCTATCAAGG
36628_at	2117	CTCTAATTTCTATCAAGGTGTCATG
36628_at	2118	CTAATTTCTATCAAGGTGTCATGGA
36628_at	2119	TTCATTACAAATGTCTCAGCATTGG
36628_at	2120	TACAAATGTCTCAGCATTGGTTAAC
36628_at	2121	AAATGTCTCAGCATTGGTTAACTAA
36628_at	2122	TGTCTCAGCATTGGTTAACTAATTT
36628_at	2123	GTCTCAGCATTGGTTAACTAATTTT
34545_at	2124	TGGCTCGGGGATAAGACCCAGCCTT
34545_at	2125	GGGATAAGACCCAGCCTTTCCACAC
34545_at	2126	CAGCCTTTCCACACATTAGTTTGTG
34545_at	2127	GCCTTTCCACACATTAGTTTGTGAT
34545_at	2128	TCCACACATTAGTTTGTGATGCTGG
34545_at	2129	CACATTAGTTTGTGATGCTGGGTCA
34545_at	2130	TGTGATGCTGGGTCATAGTGCGTCT
34545_at	2131	GCGTCTGTTTGCTCCCTGTCAAGGG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34545_at	2132	TTGCTCCCTGTCAAGGGACCAGTAA
34545_at	2133	CCCTGTCAAGGGACCAGTAACATGA
34545_at	2134	AAGGGACCAGTAACATGAGGGGTCA
34545_at	2135	ACCAGTAACATGAGGGGTTCAGAGAA
34545_at	2136	AAGGGATCAGAACTCTCGTGGGCCT
34545_at	2137	TCAGAACTCTCGTGGGCCTCCAGTG
34545_at	2138	CTCTCGTGGGCCTCCAGTGTGTCGC
34545_at	2139	CCAGTGTGTCGCAAGTTTTTGCTGT
31346_at	2140	CCGGTGTGGCGTGGAACCTCAAGCA
31346_at	2141	AGCAGGGGCAATTCCACCTCACCAG
31346_at	2142	CAGATGCAAGGCATCTCAGCACCT
31346_at	2143	AGATGCAAGGCATCTCAGCACCTC
31346_at	2144	GCTCCTGGAGCCAGGGTGCTCGTCT
31346_at	2145	GCCTTTGCCCACTGGCGCATGGG
31346_at	2146	AAAGGGGCTTCCTGCACCACACATG
31346_at	2147	GATTGAGGGCCGTCCCTGTGCTCCT
31346_at	2148	GCCGCGCAGGCAGAAGGGATCTCCC
31346_at	2149	CCGCGCAGGCAGAAGGGATCTCCCA
31346_at	2150	CTGCCCCAGCACATGGGGATTTTGC
31346_at	2151	AGGCTCCTCCAGAAGGGGCGCTCTC
31346_at	2152	CTCCTAGGTGGCATCCACACAAGGG
31346_at	2153	AAATCCGGAAGGACTGGGACGCGCA
31346_at	2154	CCACAGGGCCAAGGTGTGCTTGCGC
31346_at	2155	AGGGCCAAGGTGTGCTTGCGCCACC
40926_at	2156	TGCCCCCTAGCCAAGGAGTGTGAATT
40926_at	2157	GTCCCTTTGCCACAAGTCTGTGGGG
40926_at	2158	CTGTGGGGCAAGAGGCTGCAATATT
40926_at	2159	TGTCTGGGCTGCTAACCTGGCCTGC
40926_at	2160	TCTGGGCTGCTAACCTGGCCTGCTC
40926_at	2161	GTCCAGGCTTAAGGTGGATGCACTT
40926_at	2162	CTGTGTAGCAGCTTTAACCCACGTT
40926_at	2163	TTTAACCCACGTTTGTCTGTACAGT
40926_at	2164	CCACGTTTGTCTGTACAGTCCAGTC
40926_at	2165	TTGTCTGTACAGTCCAGTCCCGAGA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40926_at	2166	GTCTGTCACGTCCAGTCCCGAGACG
40926_at	2167	CGTCCAGTCCCGAGACGGCTGAGTG
40926_at	2168	TCCAGTCCCGAGACGGCTGAGTGAC
40926_at	2169	TCCCGAGACGGCTGAGTGACCCAA
40926_at	2170	GACGGCTGAGTGACCCCAAGAAAGG
40926_at	2171	TGAGTGACCCCAAGAAAGGCTTCCC
33803_at	2172	TTTCTACCATTTCAGAGAGGCCTTT
33803_at	2173	TGTGGCCCCTGAACAAGAATTGGAA
33803_at	2174	CCTGCCCATGGGAGCTGGTTAGAAA
33803_at	2175	CCATGGGAGCTGGTTAGAAATGCAG
33803_at	2176	TGTGTCTGCTCAGTAATTTGAGGAC
33803_at	2177	GACTGCTTCCAATTTTCTGGAATAC
33803_at	2178	GCTTCCAATTTTCTGGAATACATGA
33803_at	2179	GTTATAAGTAGCAGGCCAAGTCAGG
33803_at	2180	CCTTATTTTCAAGAAACTGAGGAAT
33803_at	2181	AGCTTTGCTCTTTGGTAGAAAAGGC
33803_at	2182	CTAGGTACACAGCTCTAGACACTGC
33803_at	2183	CCACACAGGGTCTGCAAGGTCTTTG
33803_at	2184	AGGGTCTGCAAGGTCTTTGGTTTCA
33803_at	2185	ATGAAATCCTGCTTCAGTGTATGGA
33803_at	2186	CCTGCTTCAGTGTATGGAAATAAAT
33803_at	2187	GATAATCTAGAACACAGGCCAAAATC
748_s_at	2188	AATCGACGAGCTCATCTGCGCCTTT
748_s_at	2189	TGCGCCTTTGTTTAGAACGCTTAA
748_s_at	2190	GATTCCACTAGGACCAGACTGCACC
748_s_at	2191	CGGCACACAACACTTGGTTTGCTCA
748_s_at	2192	CCAGCTCGAGAATTTGGAACGAGAA
748_s_at	2193	TGGAACAGCTGCAGGGTCCTCAGGA
748_s_at	2194	ATACGAATGGACAGCATTGGATCAA
748_s_at	2195	CAGATCGTTCTGATTCAGAGCGAGA
748_s_at	2196	GAAAGCACAGAGTTCTCCCATGGAG
748_s_at	2197	ACCAGCATCAGTGACATTGATGACC
748_s_at	2198	TATTGGGAGTGACGAGGGTACTCC
748_s_at	2199	CAGTGCCAGTGTCAAACCTTTCATTC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
748_s_at	2200	AGCATGACATAACAGTGCAGGGCAA
748_s_at	2201	TTCAGTGGGCAATTCAATACAAAC
748_s_at	2202	CAAACAATCTCTTAAATTGGGTTC
748_s_at	2203	GGTTCATGATGCAGTCTCCTCTTA
1650_g_at	2204	CCGCCTCATTGAGATGTACCGAGAC
1650_g_at	2205	ATGTACCGAGACCTCTTCCAGCAGG
1650_g_at	2206	CCGAGACCTCTTCCAGCAGGGGACC
1650_g_at	2207	GCTGTCCTCGCTGCTGAGAAGAGCC
1650_g_at	2208	CCTCGCTGCTGAGAAGAGCCACTAA
1650_g_at	2209	TGAGAAGAGCCACTAACTCGTGACC
1650_g_at	2210	GAGCCACTAACTCGTGACCTCCAGC
1650_g_at	2211	GCCGTGTGCTCCTGCCTTCCTGATC
1650_g_at	2212	TCCTGCCTTCCTGATCCTCTGTAGA
1650_g_at	2213	TGACTGCCTTCAGACCTGGCCCTGT
1650_g_at	2214	TGAGCAGGTGGGCCGTTGAGTTACC
1650_g_at	2215	AGGTGGGCCGTTGAGTTACCTCTGT
1650_g_at	2216	GGCCGTTGAGTTACCTCTGTGCTGG
1650_g_at	2217	TGAGTTACCTCTGTGCTGGATCCCG
1650_g_at	2218	TACCTCTGTGCTGGATCCCGTGCCC
1650_g_at	2219	GTCCTGCCTTGTTATTGTAAGTGCC
41617_at	2220	TTTACTGCTGAGGAGAAGGCTGCC
41617_at	2221	TTTACTGCTGAGGAGAAGGCTGCCG
41617_at	2222	TCAAGCCCGCCTTTGCTAAGCTGAG
41617_at	2223	CAAGCCCGCCTTTGCTAAGCTGAGT
41617_at	2224	GCTCCTGGGTAACGTGATGGTGATT
41617_at	2225	CTCCTGGGTAACGTGATGGTGATTA
41617_at	2226	ATGGTGATTATTCTGGCTACTCACT
41617_at	2227	GAGTTCTCTTCCAGTTTGCAGGTGT
41617_at	2228	GGTGTTCCTGTGACCCTGACACCCT
41617_at	2229	ACCCTCCTTCTGCACATGGGGACTG
41617_at	2230	CCCTCCTTCTGCACATGGGGACTGG
41617_at	2231	TCCTTCTGCACATGGGGACTGGGCT
41617_at	2232	CTGGGCTTGGCCTTGAGAGAAAGCC
41617_at	2233	GGCTTGGCCTTGAGAGAAAGCCTTC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
41617_at	2234	CACTAGCAAGCTCTCAGGCCTGGCA
41617_at	2235	CCTGGCATCATGGTGCATTTTACTG
1774_at	2236	ACCAAATCGACCAGCTTCAGCGAGA
1774_at	2237	TCGACCAGCTTCAGCGAGAGCAGCG
1774_at	2238	AGCTTCAGCGAGAGCAGCGACACCT
1774_at	2239	GCATTGAGAGGATCCGGATGGACAG
1774_at	2240	AGAGCACGGACTATCTCACAGGTGA
1774_at	2241	CGGACTATCTCACAGGTGATCTGGA
1774_at	2242	ATCTCACAGGTGATCTGGACTGGAG
1774_at	2243	ATCTGGACTGGAGCAGCAGCAGTGT
1774_at	2244	ACTGGAGCAGCAGCAGTGTGAGCGA
1774_at	2245	GCATGCAGAGCCTCGGCAGTGATGA
1774_at	2246	GTGATGAGGGCTATTCCAGCACCAG
1774_at	2247	AGGGCTATTCCAGCACCAGCATCAA
1774_at	2248	ATTCCAGCACCAGCATCAAGAGAAT
1774_at	2249	TAAAGCTGCAGGACAGTCACAAGGC
1774_at	2250	TTGGTCTCTAAGAGAGTGGGCACTG
1774_at	2251	GGCACTGCGGCTGTCTCCTTGAAGG
40990_at	2252	GCTGTGTGCCCCAGTTTGAGAAAGTG
40990_at	2253	ATTTAACCATCGTTGCTGGTATTTT
40990_at	2254	CGTTGCTGGTATTTTTCATAGGCATT
40990_at	2255	TTTTCATAGGCATTGCATTGCTGCA
40990_at	2256	ATATTTGGGATATGCCTGGCCCAGA
40990_at	2257	TGCCTGGCCCAGAATTTGGTTAGCG
40990_at	2258	ATATCGAAGCTGTCAGGGCGAGCTG
40990_at	2259	GTCAGGGCGAGCTGGTAGACCCCCT
40990_at	2260	CTGCAAGACACTGGACAGACCCAGC
40990_at	2261	GCGTGCCGAAGTATCTTCGAGCTG
40990_at	2262	CTGATCTTCGAGCTGCATGGACCTA
40990_at	2263	GAGCTGCATGGACCTAATCACAGAT
40990_at	2264	GACCTAATCACAGATGCAGCCTGCA
40990_at	2265	GGAAATGCTGCTCACTGACAGAATT
40990_at	2266	CGTGAATCTCTACTGTAGCCATGAA
40990_at	2267	ACCAGATGTACTTGAATGTGCAGAA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34798_at	2268	AAAGGTTTCAGGCATTCCTAGCCGAG
34798_at	2269	GGTTCAGGCATTCCTAGCCGAGTGT
34798_at	2270	GCGGCTGCAGTCTACAAACTTTGCC
34798_at	2271	GCAGTCTACAAACTTTGCCCTGGCC
34798_at	2272	CTGTGCTGCCCTGAAGAATGGCGCC
34798_at	2273	TACCTGATTTCTTCAGGGCTGCTGG
34798_at	2274	CACACTGGTTCTCAATGAAAAATAG
34798_at	2275	CACTGGTTCTCAATGAAAAATAGTG
34798_at	2276	AGTCCACAGGAAGAGGTTGAACTAA
34798_at	2277	AGAAGATAGCTGACCAGCTGGAAGA
34798_at	2278	AGAGCTTACTGGAATCCAGCAGGGT
34798_at	2279	TACTGGAATCCAGCAGGGTTTTCTG
34798_at	2280	GCCCAAGGATTTGCAAGCTGAAGCT
34798_at	2281	GCAAGCTGAAGCTCTCTGCAAACTT
34798_at	2282	TCTCTGCAAACTTGATAGGAGAGTA
34798_at	2283	TGACACACTGATCCTGCCAGAAAAT
35674_at	2284	CCTATTTGAGGGTGTCTGTCTGGAG
35674_at	2285	CTGTCTGGAGACTTAGAGTTTGTCA
35674_at	2286	CCTCCCATGTGCAGACAGTGTGTCT
35674_at	2287	CATGTGCAGACAGTGTGTCTTTATA
35674_at	2288	TTTCCCCAATGATGTTCGGTAATTTC
35674_at	2289	TCCCCAATGATGTTCGGTAATTCTG
35674_at	2290	AATTTCTGATGTTTCTGAAGTTCCC
35674_at	2291	CACCCAGTGTGACAACCCTCGGTGT
35674_at	2292	ACCCAGTGTGACAACCCTCGGTGTG
35674_at	2293	CGGTGTGGATATACCCCCGTGGACT
35674_at	2294	ATACCCCCGTGGACTCATGGCTCTT
35674_at	2295	TCTCTGTTGCAAACTCAGCTAAGT
35674_at	2296	TCTGTTGCAAACTCAGCTAAGTTC
35674_at	2297	GCAAACTCAGCTAAGTTCCTGCTT
35674_at	2298	TAAGTTCCTGCTTCCACCTTGATGT
35674_at	2299	CCTGCTTCCACCTTGATGTTGAAAT
1368_at	2300	CACATTCCTAGTTCCTCCGTGAACTT
1368_at	2301	CCGTGAACTTCCTTTGACTTATTGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1368_at	2302	TGAACTTCCTTTGACTTATTGTCCC
1368_at	2303	CTTTTAATGCCTTCCACATTAATTA
1368_at	2304	TTAATGCCTTCCACATTAATTAGAT
1368_at	2305	CCTTCCACATTAATTAGATTTTCTT
1368_at	2306	TAAAGATGCCCTAAGTGTTGAAGAA
1368_at	2307	TGCCCTAAGTGTTGAAGAAGAGTTT
1368_at	2308	TATTAAAGCACCAAATTCATGTACA
1368_at	2309	TAAAGCACCAAATTCATGTACAGCA
1368_at	2310	AGCACCAAATTCATGTACAGCATGC
1368_at	2311	AAATTCATGTACAGCATGCATCACG
1368_at	2312	TTCATGTACAGCATGCATCACGGAT
1368_at	2313	ATGTACAGCATGCATCACGGATCAA
1368_at	2314	ATGCATCACGGATCAATAGACTGTA
1368_at	2315	ATAGACTGTACTTATTTTCCAATAA
430_at	2316	TAGTCACCAATGCAGCAGGAGGGCT
430_at	2317	GAGATCGTTTCCCTGCCATGTCTGA
430_at	2318	CTGCCATGTCTGATGCCTACGACCG
430_at	2319	TGTCTGATGCCTACGACCGGACTAT
430_at	2320	GCACCTATGTGATGGTGGCAGGCCC
430_at	2321	CTGTGGCAGAATGTCGTGTGCTGCA
430_at	2322	CAGAATGTCGTGTGCTGCAGAAGCT
430_at	2323	CTGTTGGCATGAGTACAGTACCAGA
430_at	2324	TCGTTGCACGGCACTGTGGACTTCG
430_at	2325	GAGTCTTTGGCTTCTCACTCATCAC
430_at	2326	TTGGCTTCTCACTCATCACTAACAA
430_at	2327	TCATCACTAACAAGGTCATCATGGA
430_at	2328	CAGCTGGCAAACAAGCTGCACAGAA
430_at	2329	GCAAACAAGCTGCACAGAAATTGGA
430_at	2330	TTGTCTCCATTCTTATGGCCAGCAT
430_at	2331	CCATTCTTATGGCCAGCATTCCACT
39248_at	2332	CTTCTACAGGCTTTTGGGAAGTAGG
39248_at	2333	GGCCACAGCTTAGGTTTGGAGCTCT
39248_at	2334	CTTAGGTTTGGAGCTCTGGATGTAC
39248_at	2335	TGGAGCTCTGGATGTACATACATAA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39248_at	2336	AGCAGTGGGACGTGTTTCTGTCATA
39248_at	2337	CAGTGGGACGTGTTTCTGTCATAAT
39248_at	2338	TGGGACGTGTTTCTGTCATAATGCA
39248_at	2339	TCTGTCATAATGCAGGCATGAAGGG
39248_at	2340	CTGTCATAATGCAGGCATGAAGGGT
39248_at	2341	AGCAGATGTTACAGTCTTAGGGATC
39248_at	2342	AGATGTTACAGTCTTAGGGATCCGG
39248_at	2343	ATGTTACAGTCTTAGGGATCCGGGA
39248_at	2344	TGTTACAGTCTTAGGGATCCGGGAT
39248_at	2345	TAGAAAGGGTCGTCACCTCTTAAAT
39248_at	2346	AGGGTCGTCACCTCTTAAATCCTCT
39248_at	2347	GGGTCGTCACCTCTTAAATCCTCTA
33932_at	2348	TCGCTTAAGGACAGCAGGAACCATC
33932_at	2349	ACCATCTGCCTTGAGACCTTTAAAG
33932_at	2350	CCTTTAAAGACTTCCCTCAGATGGG
33932_at	2351	AAGACCATTGCAATTGGAAAAGTTC
33932_at	2352	TGAAACTGGTTCCAGAGAAAGACTA
33932_at	2353	ATGACCCTGCACAATACTGTGAGGA
33932_at	2354	CTGCACAATACTGTGAGGAAAATTG
33932_at	2355	AAATTGACTGCAGAAGCCTACTTCA
33932_at	2356	ATTGACTGCAGAAGCCTACTTCACA
33932_at	2357	TCTCCCCATATTTTGCAAAGAGGAA
33932_at	2358	TCCCCATATTTTGCAAAGAGGAAAT
33932_at	2359	GGAAATTCACAGCAAAAGTCCACAT
33932_at	2360	GCTTTCTCATATTGAGAGCTCTGCT
33932_at	2361	GCCACTGTTGAATTTTCCCAAGAT
33932_at	2362	TATTTAGTATTTTCCCCCAGGCAG
33932_at	2363	TGTGTGTGCACATGTTACAAAGGCA
35767_at	2364	CTATGGGACAGCTTTACGAGAAGGA
35767_at	2365	AGATGGATTCTTATATGTGGCCTAC
35767_at	2366	AGAGAACACTTTTGGCTTCTGAGGG
35767_at	2367	CTTCTGAGGGCCATTGCTGGGCTAG
35767_at	2368	AGGTGCACCGTAACTGCTTGTGTAT
35767_at	2369	TCACATAGACCTATTAGTGCATTTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35767_at	2370	CCTATTAGTGCATTTGTAACCTGGAT
35767_at	2371	TCTTTTTGTGCATTGTCCTCATGCC
35767_at	2372	CATGCCTGTATTCTCCAGGAACTT
35767_at	2373	AAATCCTTAGCAGTCAGAACACTTG
35767_at	2374	AATCCTTAGCAGTCAGAACACTTGC
35767_at	2375	TAGCAGTCAGAACACTTGCTTCACT
35767_at	2376	GTCAGAACACTTGCTTCACTAGAAT
35767_at	2377	TAGAATATGCCAACTGCCAATCATG
35767_at	2378	CTGAGCTAATTTGTTCTCTTTCTG
35767_at	2379	GTTCTCTTTCTGAACTATTAAGG
33516_at	2380	CTGTCAATGCCCTGTGGGGCAAAGT
33516_at	2381	GTCAATGCCCTGTGGGGCAAAGTGA
33516_at	2382	GACACTTTCTTCTGACATAACAGTG
33516_at	2383	TGGCTCACAAGTACCATTGAGATCC
33516_at	2384	GCTCACAAGTACCATTGAGATCCTG
33516_at	2385	CAACCTCAAACAGACACCATGGTGC
33516_at	2386	CTTGGAACACAATGCCTACTTCAA
33516_at	2387	TTGGGAACACAATGCCTACTTCAAG
33516_at	2388	GAACACAATGCCTACTTCAAGGGTA
33516_at	2389	AACACAATGCCTACTTCAAGGGTAT
33516_at	2390	CACAATGCCTACTTCAAGGGTATGG
33516_at	2391	ATGCCTACTTCAAGGGTATGGCTTC
33516_at	2392	ACACCATGGTGCATCTGACTCCTGA
33516_at	2393	TCTGACTCCTGAGGAGAAGACTGCT
33516_at	2394	GGAGAAGACTGCTGTCAATGCCCTG
33516_at	2395	GACTGCTGTCAATGCCCTGTGGGGC
40120_at	2396	CTTTTAGGTAACCTGGCTTTCCTGCT
40120_at	2397	GGTAACCTGGCTTTCCTGCTGGTCCG
40120_at	2398	CCTGCTGGTCCGTGCGGGAAATTCA
40120_at	2399	GTCCGTGCGGGAAATTCAAGTCTTGA
40120_at	2400	ACAGCCCTTGGCTTGTGTTATCGGA
40120_at	2401	GTTACAGGTGACACCTTGTGTTGTG
40120_at	2402	AGGTGACACCTTGTGTTGTGGCTGGC
40120_at	2403	GTGTAAAGCTCTGCTGGAGGTCTTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40120_at	2404	CACCCTGGCAGAGGAGTTTACCTAC
40120_at	2405	CTACAACCCCTTCATGAGAGTGAGG
40120_at	2406	CCCCTTCATGAGAGTGAGGGAGAAG
40120_at	2407	CCCTTCATGAGAGTGAGGGAGAAGA
40120_at	2408	CAGGTGAGACGGACCCGGTGACCAC
40120_at	2409	AGGACCAGTTCAAGATGCCCCGGGA
40120_at	2410	CTTCAGCGGATTTGGGGATTAGGCT
40120_at	2411	GATTAGGCTCTTTTAGGTAAGTGGC
31380_at	2412	TCCAGACGCCCTCTGAGCGAGGGCG
31380_at	2413	CCTCTGTTCTGGTGGCCCCAGCTGT
31380_at	2414	TCTGGTGGCCCCAGCTGTGACTGAG
31380_at	2415	GGAGACCAGGCTTCCCAAACCAAGT
31380_at	2416	CAGAGGACAGTGCTGACCCCAGGAA
31380_at	2417	AGAGGACAGTGCTGACCCCAGGAAG
31380_at	2418	GATGCTGGCCCCAAAAGCCTTACGG
31380_at	2419	CAAAGGAGGGCCTCAGAGACAGCGC
31380_at	2420	GGCCTCAGAGACAGCGCGAGTAGCA
31380_at	2421	ATTCCTGCTTAATGTCAGTCTACAG
31380_at	2422	ATGTCAGTCTACAGGCCTTTCAGGA
31380_at	2423	GGAATCGTACATTTTGCTTGCGTGC
31380_at	2424	TTTGCTTGCGTGCTGGGACAGCTAG
31380_at	2425	GGACAGCTAGGCTGAGATGCACCAA
31380_at	2426	CCTTCACTGGAGACCGGAATTGAGA
31380_at	2427	AGTTCAGAGGGTGTCGTCCTGCAGT
35379_at	2428	GTGCCACTGGGCTTCCTGGAAGGCC
35379_at	2429	GAATTCGTGGCCTTCCGGGCATTAA
35379_at	2430	AATTCGTGGCCTTCCGGGCATTAAAG
35379_at	2431	CCCCCTGGTGCTCTTGGTTTGAGGG
35379_at	2432	GCTCTTGGTTTGAGGGGACCTAAAG
35379_at	2433	AGCGTGGCCCTCCAGGAAGAGGTCC
35379_at	2434	GCGTGGCCCTCCAGGAAGAGGTCCC
35379_at	2435	ATAGGTCTCCAGGTGACCCAGGCC
35379_at	2436	TCCTGGAGTGCCTGGACCCCCGGGA
35379_at	2437	TGGAGTGCCTGGACCCCCGGGACCT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35379_at	2438	GACCTCCTGGGCTTCCCGGTTTCTG
35379_at	2439	GGCTTCCCGGTTTCTGTGAGCCAGC
35379_at	2440	TTCCCGGTTTCTGTGAGCCAGCCTC
35379_at	2441	CCGGTTTCTGTGAGCCAGCCTCCTG
35379_at	2442	CTCCTGCACCATGCAGGCTGGTCAG
35379_at	2443	AGCATTTAACAAAGGGCCTGACCCT
38138_at	2444	TCCAGCCCTACAGAGACTGAGCGGT
38138_at	2445	CCTACAGAGACTGAGCGGTGCATCG
38138_at	2446	GCTGTCTTCCAGAAGTATGCTGGAA
38138_at	2447	CTTCCAGAAGTATGCTGGAAAGGAT
38138_at	2448	CTTCATGAATACAGAACTAGCTGCC
38138_at	2449	GCCTTCACAAAGAACCAGAAGGACC
38138_at	2450	AAGGACCCTGGTGTCTTGACCGCA
38138_at	2451	ACCCTGGTGTCTTGACCGCATGAT
38138_at	2452	ACAGTGATGGTCAGCTAGATTTCTC
38138_at	2453	GAATTTCTTAATCTGATTGGTGGCC
38138_at	2454	CTTAATCTGATTGGTGGCCTAGCTA
38138_at	2455	CTAGCTATGGCTTGCCATGACTCCT
38138_at	2456	ATGGCTTGCCATGACTCCTTCCTCA
38138_at	2457	GCCATGACTCCTTCCTCAAGGCTGT
38138_at	2458	GAAGCGGACCTGAGGACCCCTTGGC
38138_at	2459	ACCTGCCAATAGTAATAAAGCAATG
355_s_at	2460	TTTGAAGAGGGTGCAGCCCAGATGA
355_s_at	2461	GACCTGCACCCCTGATGTGGCATAT
355_s_at	2462	CCTCATCTTTGACGTGGAGCTGCTC
355_s_at	2463	ACTGGGACGGCTCCTGCTTTTGGGG
355_s_at	2464	TTGGGGCTCTTGATCAGTGTGCTAA
355_s_at	2465	CATCATCCATTCTCTCTGCCCAAGT
355_s_at	2466	CCAAGTTGCTCTGTATGTGTTCGTC
355_s_at	2467	TTGCTTGAGGAACTTCGGTTGCAG
355_s_at	2468	ATTTTGTGTGATGCATGTAGTAGCC
355_s_at	2469	CTTTCCTGATAACAGAACACAGATC
355_s_at	2470	CAGATCTCTTGTTTCGCACAATCTAC
355_s_at	2471	TCACTTAAACCACACACACAAGGTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
355_s_at	2472	CAAGGTGCTCAGACATGAAATGTAC
355_s_at	2473	GTACCGTACACAGAGGGACTTGAGC
355_s_at	2474	GAGCCAGTTACCTTTGCTGTCACTT
355_s_at	2475	TAGCTGCTCACTTAAACAATGTCCT
39331_at	2476	ATCAATCGTGCATCCTTAGTGAAC
39331_at	2477	CGTGCATCCTTAGTGAACCTTCTGTT
39331_at	2478	TCCTTAGTGAACCTTCTGTTGTCCTC
39331_at	2479	TTAGTGAACCTTCTGTTGTCCTCAAG
39331_at	2480	GTGAACCTTCTGTTGTCCTCAAGCAT
39331_at	2481	CAAGCATGGTCTTTCTACTTGTA
39331_at	2482	TGGTCTTTCTACTTGTA
39331_at	2483	TTCTACTTGTA
39331_at	2484	GTA
39331_at	2485	AA
39331_at	2486	AT
39331_at	2487	AG
39331_at	2488	GT
39331_at	2489	TT
39331_at	2490	GC
39331_at	2491	AAT
36045_at	2492	CTA
36045_at	2493	TA
36045_at	2494	A
36045_at	2495	AT
36045_at	2496	TT
36045_at	2497	TG
36045_at	2498	GT
36045_at	2499	TT
36045_at	2500	TG
36045_at	2501	GT
36045_at	2502	TT
36045_at	2503	TT
36045_at	2504	TC
36045_at	2505	CA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36045_at	2506	ACCCCTATGGATAGGTTTTACCTG
36045_at	2507	CCCCTATGGATAGGTTTTACCTGT
39145_at	2508	CTGGGATCAGACACCCCTTCACGTG
39145_at	2509	CCACACAAATGCAAGCTCACCAAGG
39145_at	2510	CACAAATGCAAGCTCACCAAGGTCC
39145_at	2511	AAATGCAAGCTCACCAAGGTCCCCT
39145_at	2512	ACCCGCCATGGGAGTGTGCTCAGGA
39145_at	2513	CAGAATCTCCAATAGAGGACTGAGC
39145_at	2514	ATCTCCAATAGAGGACTGAGCACTG
39145_at	2515	CACCGCGGGATTTCGGACGAGGATT
39145_at	2516	CTCGCTCAGGGATCCCCCTTTGAGG
39145_at	2517	TTAGGGTCCCAGTTCCTCAGTGAAG
39145_at	2518	CCAGTTCCCAGTGGAAGAAACAGGC
39145_at	2519	TTCCCAGTGGAAGAAACAGGCCAGG
39145_at	2520	CGTGCCGAGCTGAGGCAGATGTTCC
39145_at	2521	TGAGGCAGATGTTCCACAGTGACC
39145_at	2522	GAAGAGGCCCTGAGTCCTGGGATCA
39145_at	2523	AGTCCTGGGATCAGACACCCCTTCA
39423_f_at	2524	CCTGTCTGCATCTGACTGAGCAGAA
39423_f_at	2525	CTGTCTGCATCTGACTGAGCAGAAC
39423_f_at	2526	GTCTGCATCTGACTGAGCAGAACAA
39423_f_at	2527	CTGCATCTGACTGAGCAGAACAAAT
39423_f_at	2528	GCATCTGACTGAGCAGAACAAATCG
39423_f_at	2529	CATCTGACTGAGCAGAACAAATCGT
39423_f_at	2530	ATCTGACTGAGCAGAACAAATCGTC
39423_f_at	2531	AGCAGAACAAATCGTCAGGTGCCTG
39423_f_at	2532	CAGAACAAATCGTCAGGTGCCTGGA
39423_f_at	2533	AGAACAAATCGTCAGGTGCCTGGAG
39423_f_at	2534	GAACAAATCGTCAGGTGCCTGGAGC
39423_f_at	2535	CAAATCGTCAGGTGCCTGGAGCAAA
39423_f_at	2536	TCGTCAGGTGCCTGGAGCAAAAAGG
39423_f_at	2537	CGTCAGGTGCCTGGAGCAAAAAGGA
39423_f_at	2538	GTCAGGTGCCTGGAGCAAAAAGGAA
39423_f_at	2539	TCAGGTGCCTGGAGCAAAAAGGAAA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38598_at	2540	GGAAGGCACGAAGTCTCTAAAGCAT
38598_at	2541	AAGGCACGAAGTCTCTAAAGCATCC
38598_at	2542	AGGCACGAAGTCTCTAAAGCATCCA
38598_at	2543	GCACGAAGTCTCTAAAGCATCCAGA
38598_at	2544	CACGAAGTCTCTAAAGCATCCAGAA
38598_at	2545	ACGAAGTCTCTAAAGCATCCAGAAG
38598_at	2546	CGAAGTCTCTAAAGCATCCAGAAGA
38598_at	2547	GAAGTCTCTAAAGCATCCAGAAGAC
38598_at	2548	AAGTCTCTAAAGCATCCAGAAGACC
38598_at	2549	AGTCTCTAAAGCATCCAGAAGACCC
38598_at	2550	GTCTCTAAAGCATCCAGAAGACCCC
38598_at	2551	GAAGACCCCTACACCAGGGTCTGGT
38598_at	2552	TACACCAGGGTCTGGTCCGCTCCTA
38598_at	2553	ACACCAGGGTCTGGTCCGCTCCTAT
38598_at	2554	CACCAGGGTCTGGTCCGCTCCTATT
38598_at	2555	ACCAGGGTCTGGTCCGCTCCTATTC
33799_at	2556	CCCGGAGTGCTTATCTTAAAATTGC
33799_at	2557	AAATTGCAGATTTAGGGAGCCTGCC
33799_at	2558	ATTTAGGGAGCCTGCCAATTTAACA
33799_at	2559	CAGGTGATTCTTTTCAACAGTAATG
33799_at	2560	AGGTGCTTTAAGGTTGCCCTCTGCC
33799_at	2561	GCCCTCTGCCGATACTGTTTGTCTT
33799_at	2562	TGCCGATACTGTTTGTCTTTCTACT
33799_at	2563	CCGATACTGTTTGTCTTTCTACTGT
33799_at	2564	CTAGAACTATAGATCCACATGAACG
33799_at	2565	ACTATAGATCCACATGAACGCACGC
33799_at	2566	TGGATTGCCTAGGAAAGCAAGTCAT
33799_at	2567	GATTGCCTAGGAAAGCAAGTCATAT
33799_at	2568	AGTCATATGGCCATTGATAGTTCTC
33799_at	2569	TGGCCATTGATAGTTCTCATGTAAT
33799_at	2570	AGTTCTCATGTAATTAGTTTTGCTC
33799_at	2571	TTGCTCACCAGTAGTACAGATGACC
34319_at	2572	ATAGACGTCTTTTCCCGATATTCGG
34319_at	2573	TTTCCCGATATTCGGGCAGCGAGG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34319_at	2574	GCAGCGAGGGCAGCACGCAGACCCT
34319_at	2575	GCACGCAGACCCTGACCAAGGGGGA
34319_at	2576	AGCTACCAGGCTTCCTGCAGAGTGG
34319_at	2577	CCAGGCTTCCTGCAGAGTGGAAAAG
34319_at	2578	GCTTCCTGCAGAGTGGAAAAGACAA
34319_at	2579	TCAAGGACCTGGACGCCAATGGAGA
34319_at	2580	CAGGTGGACTTCAGTGAGTTCATCG
34319_at	2581	GACTTCAGTGAGTTCATCGTGTTTCG
34319_at	2582	CTTCAGTGAGTTCATCGTGTTTCGTG
34319_at	2583	TGTCACAAGTACTTTGAGAAGGCAG
34319_at	2584	AGTACTTTGAGAAGGCAGGACTCAA
34319_at	2585	TGTTGGCAATTATTCCCCTAGGCTG
34319_at	2586	CACCATGACGGAAGTAGAGACAGCC
34319_at	2587	ATGATCATAGACGTCTTTTCCCGAT
36113_s_at	2588	CCTCTCCGAGCGTAAGAAGCCTCTG
36113_s_at	2589	CGTAAGAAGCCTCTGGACATTGACT
36113_s_at	2590	GAGAAAGCCCAGGAGCTGTCGGACT
36113_s_at	2591	AAAGCCCAGGAGCTGTCGGACTGGA
36113_s_at	2592	AAGCCCAGGAGCTGTCGGACTGGAT
36113_s_at	2593	GCCCAGGAGCTGTCGGACTGGATCC
36113_s_at	2594	AGGAGCTGTCGGACTGGATCCACCA
36113_s_at	2595	GGAGCTGTCGGACTGGATCCACCAG
36113_s_at	2596	CTGTCGGACTGGATCCACCAGCTGG
36113_s_at	2597	TCGGACTGGATCCACCAGCTGGAGT
36113_s_at	2598	CGGACTGGATCCACCAGCTGGAGTC
36113_s_at	2599	GGACTGGATCCACCAGCTGGAGTCT
36113_s_at	2600	ACTGGATCCACCAGCTGGAGTCTGA
36113_s_at	2601	GCCTGGGAGTGTTTGTCCCATCGGT
36113_s_at	2602	GTGTTTGTCCCATCGGTAGCTTGAA
36113_s_at	2603	TGTCCCATCGGTAGCTTGAAATAAA
40848_g_at	2604	CAATAGCAAACAACGGAAGAGACGG
40848_g_at	2605	GCAAACAACGGAAGAGACGGGCAGA
40848_g_at	2606	CAAACAACGGAAGAGACGGGCAGAG
40848_g_at	2607	AGAGACGGGCAGAGTTGAAGCAACA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40848_g_at	2608	CTTTATAGAATGTCAACCAAAGAGT
40848_g_at	2609	TTATAGAATGTCAACCAAAGAGTGC
40848_g_at	2610	GAATGTCAACCAAAGAGTGCCCTCC
40848_g_at	2611	AATGTCAACCAAAGAGTGCCCTCCT
40848_g_at	2612	CATCTCATCACAACGCATGTCTGTG
40848_g_at	2613	ACAACGCATGTCTGTGACCTTTGGT
40848_g_at	2614	ATGTCTGTGACCTTTGGTAATCATT
40848_g_at	2615	GTGACCTTTGGTAATCATTTACAGT
40848_g_at	2616	GTAATCATTTACAGTGCCACACGGA
40848_g_at	2617	AGTGCCACACGGAACCCTGTATTTT
40848_g_at	2618	GTGCCACACGGAACCCTGTATTTTG
40848_g_at	2619	CACGGAACCCTGTATTTTGCACACA
2094_s_at	2620	TCCCAGCTGCACTGCTTACACGTCT
2094_s_at	2621	CTTACACGTCTTCCTTCGTCTTCAC
2094_s_at	2622	AGCAGCAGCAATGAGCCTTCCTCTG
2094_s_at	2623	AGTCTGCTTTGCAGACCGAGATTGC
2094_s_at	2624	TAGAGTTCATCCTGGCAGCTCACCG
2094_s_at	2625	CCTGGGCTTCCCAGAAGAGATGTCT
2094_s_at	2626	ATGTCTGTGGCTTCCCTTGATCTGA
2094_s_at	2627	CCTTGATCTGACTGGGGGCCTGCCA
2094_s_at	2628	CCCAAGCCCTCAGTGGAACCTGTCA
2094_s_at	2629	TGGAACCTGTCAAGAGCATCAGCAG
2094_s_at	2630	AGCCCTTTGATGACTTCCTGTTCCC
2094_s_at	2631	TTCCTGTTCCCAGCATCATCCAGGC
2094_s_at	2632	GACCTATCTGGGTCCTTCTATGCAG
2094_s_at	2633	CTATGCAGCAGACTGGGAGCCTCTG
2094_s_at	2634	GCCCATGGCCACAGAGCTGGAGCCC
2094_s_at	2635	GAGCCCCTGTGCACTCCGGTGGTCA
37185_at	2636	CTCACCCTAAACTAAGCGTGCTGC
37185_at	2637	AAACTAAGCGTGCTGCTTCTGCAAA
37185_at	2638	AGCGTGCTGCTTCTGCAAAAGATTT
37185_at	2639	CTGCTTCTGCAAAAGATTTTTGTAG
37185_at	2640	TTTTTGTAGATGAGCTGTGTGCCTC
37185_at	2641	TTTGTAGATGAGCTGTGTGCCTCAG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37185_at	2642	GTGTGCCTCAGAATTGCTATTTCAA
37185_at	2643	GCCTCAGAATTGCTATTTCAAATTG
37185_at	2644	TCATTTGGTCTTCTAAAATGGGATC
37185_at	2645	TTGGTCTTCTAAAATGGGATCATGC
37185_at	2646	GGGATCATGCCCATTAGATTTTCC
37185_at	2647	GGATCATGCCCATTAGATTTTCT
37185_at	2648	TTGCTCACTGCCTATTTAATGTAGC
37185_at	2649	GCTCACTGCCTATTTAATGTAGCTA
37185_at	2650	GCCTTTAATTGTTCTCATAATGAAG
37185_at	2651	AGTAGGTATCCCTCCATGCCCTTCT
35714_at	2652	CTCCGTGGTGATGGAACGCATCCGG
35714_at	2653	GCATCCGGATGGACATTCGCAAAGT
35714_at	2654	GCACTGGGGACCTGTTTGCTGCCAT
35714_at	2655	TGGCGTGGACACACAAGCACCCCAA
35714_at	2656	TGGCCTGTGAGAAGACCGTGTCTAC
35714_at	2657	TGTCTACCTTGCACCACGTTCTGCA
35714_at	2658	CCTTGCACCACGTTCTGCAGAGGAC
35714_at	2659	ACCACGTTCTGCAGAGGACCATCCA
35714_at	2660	AGAGGACCATCCAGTGTGCAAAAGC
35714_at	2661	CCATCCAGTGTGCAAAAGCCCAGGC
35714_at	2662	CCAGTGTGCAAAAGCCCAGGCCGGG
35714_at	2663	AAAGGGACATCGAGGACCCAGAGAT
35714_at	2664	GGGACATCGAGGACCCAGAGATCGT
35714_at	2665	TCGAGGACCCAGAGATCGTCGTCCA
35714_at	2666	AGATCGTCGTCCAGGCCACGGTGCT
35714_at	2667	CCCGTGACACGCAGCGCGTTGGTGT
40951_at	2668	AAAGTCAGTGACATGCCCATGCGAG
40951_at	2669	AGTGACATGCCCATGCGAGTACCTG
40951_at	2670	GTGACATGCCCATGCGAGTACCTGA
40951_at	2671	CATGCCCATGCGAGTACCTGAGGAA
40951_at	2672	GCCCATGCGAGTACCTGAGGAAGGT
40951_at	2673	CCATGCGAGTACCTGAGGAAGGTGA
40951_at	2674	GTCTCAGCTGCCACACATCTCATAG
40951_at	2675	AGCTGCCACACATCTCATAGCCGGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40951_at	2676	CACACATCTCATAGCCGGTGATGCT
40951_at	2677	CTTACGCAGTCACAGTACTGGCTTC
40951_at	2678	TTACGCAGTCACAGTACTGGCTTCT
40951_at	2679	CAGTCACAGTACTGGCTTCTTCCTC
40951_at	2680	TTTCTTTCCATACAAGTGGCTTAGG
40951_at	2681	TTTCCATACAAGTGGCTTAGGGATG
40951_at	2682	TGGATGAAAACCACTATCTTCTGTC
40951_at	2683	GATGAAAACCACTATCTTCTGTCAG
37187_at	2684	CGCCTAATGTGTTTGAGCATCACTT
37187_at	2685	GTTTGAGCATCACTTAGGAGAAGTC
37187_at	2686	TAGGTCAAACCCAAGTTAGTTCAAT
37187_at	2687	GGTTTGCAGATATTCTCTAGTCATT
37187_at	2688	TGCAGATATTCTCTAGTCATTTGTT
37187_at	2689	GCAGATATTCTCTAGTCATTTGTTA
37187_at	2690	TTTCTTCGTGATGACATATCACATG
37187_at	2691	TTCTTCGTGATGACATATCACATGT
37187_at	2692	CGTGATGACATATCACATGTCAGCC
37187_at	2693	TGACATATCACATGTCAGCCACTGT
37187_at	2694	ACATATCACATGTCAGCCACTGTGA
37187_at	2695	CATATCACATGTCAGCCACTGTGAT
37187_at	2696	CCACTGTGATAGAGGCTGAGGAATC
37187_at	2697	AATGATTTCACAGTGTGTGGTCAAC
37187_at	2698	TGTGTGGTCAACATTTCTCATGTTG
37187_at	2699	ACATTTCTCATGTTGAAGCTTTAAG
33506_at	2700	CCTACTTTGAGCAGTTTAAGGAAGT
33506_at	2701	GGAAGTTTTGCCTGAGGATTGCCTG
33506_at	2702	CTGAGGATTGCCTGCCTCGGTCTCG
33506_at	2703	GGATTGCCTGCCTCGGTCTCGCAGT
33506_at	2704	GAGTGCATGCGCAGCATTGGAACAC
33506_at	2705	CATGCGCAGCATTGGAACACGGGAG
33506_at	2706	CAGCATTGGAACACGGGAGGTAGTC
33506_at	2707	TGGAACACGGGAGGTAGTCACCCAG
33506_at	2708	AGGTAGTCACCCAGAAAACTTGAG
33506_at	2709	CCCAGAAAACTTGAGCGGCCTGGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
33506_at	2710	ACTTGAGCGGCCTGGTGCCCATCCG
33506_at	2711	GGCCTGGTGCCCATCCGAGACTTAA
33506_at	2712	ATCCGAGACTTAAGGCTAGACCCCA
33506_at	2713	GTTCCATCCCTTTATTAGCTCTGAG
33506_at	2714	CTCTGAGCCCCAATTTACTGATTGT
33506_at	2715	TTACTGATTGTGTGGCTCTTTCTGA
34430_at	2716	CGAGCAGGTCTTCAATGAGGCTCCT
34430_at	2717	CTTCAATGAGGCTCCTGGCATCAGC
34430_at	2718	GAGGCTCCTGGCATCAGCTGCAACC
34430_at	2719	GCATCAGCTGCAACCCAGTGCAGGG
34430_at	2720	GCCTGGCCCCCGATATGTTCTTCTG
34430_at	2721	AAACTGCGGCTGCTGCTGGAGAAGC
34430_at	2722	GAAGCTGAGCAGGTTCCATGCCAAG
34430_at	2723	TGAGCACCCCAGCTGGGGCCAGGCT
34430_at	2724	CTGGGTCGCCCTGGACTGTGTGCTC
34430_at	2725	TGGGTCGCCCTGGACTGTGTGCTCA
34430_at	2726	CTGGACTGTGTGCTCAGGAGCCCTG
34430_at	2727	GCCCTGGGAGGCTCTGGAGCCCCT
34430_at	2728	CTGGAGCCCCTGTACTTGTCTCTTG
34430_at	2729	TGTACTTGCTCTTGATGCCTGGCGG
34430_at	2730	GTACTTGCTCTTGATGCCTGGCGGG
34430_at	2731	CTGCCTCTCTGCAGGTCCCTAATAA
40062_s_at	2732	ACATTTCCCGCAACAAGGAGCAGGG
40062_s_at	2733	CATTTCCCGCAACAAGGAGCAGGGC
40062_s_at	2734	TTGGCTTTAGCCATAACCAGGGTGAG
40062_s_at	2735	TGGCTTTAGCCATAACCAGGGTGAGT
40062_s_at	2736	GGCTTTAGCCATAACCAGGGTGAGTT
40062_s_at	2737	GCTTTAGCCATAACCAGGGTGAGTTA
40062_s_at	2738	CTTTAGCCATAACCAGGGTGAGTTAA
40062_s_at	2739	GCCATAACCAGGGTGAGTTAAAGAGA
40062_s_at	2740	CCATAACCAGGGTGAGTTAAAGAGAG
40062_s_at	2741	CTGTTAATAAACAGCTCTAACACGG
40062_s_at	2742	TGTTAATAAACAGCTCTAACACGGC
40062_s_at	2743	GTTAATAAACAGCTCTAACACGGCC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40062_s_at	2744	TAATAAACAGCTCTAACACGGCCAG
40062_s_at	2745	TAAACAGCTCTAACACGGCCAGGCT
40062_s_at	2746	AACAGCTCTAACACGGCCAGGCTGG
40062_s_at	2747	TCTAACACGGCCAGGCTGGGCTCTG
37179_at	2748	CTAGTCCGGGACATCCGACGACGGG
37179_at	2749	AAGCTGGAAACCATTGTGCAGCTGG
37179_at	2750	AGCTGGAAACCATTGTGCAGCTGGA
37179_at	2751	AGCTGGAGCGGCTGACCAATGAACG
37179_at	2752	CAGACCGGACCCTGGAGGTCATGCG
37179_at	2753	CGGACCCTGGAGGTCATGCGCCAAC
37179_at	2754	CGCCAACAGCTGACAGAGCTGTACC
37179_at	2755	AGAGCTGTACCGTGACATTTTCCAG
37179_at	2756	CAGGCAACAGCTACTCTCCTGAAGA
37179_at	2757	ACGCGCTGCAACAGGCTGCCGATGG
37179_at	2758	ATGGAGGCCACAGACTGAGCTGGCC
37179_at	2759	TGATGGGATTTTCCTTCATTCCCTTC
37179_at	2760	ACCCTGAGTCCCAGAAGGAGCTGAG
37179_at	2761	AGTTCTCTAGACCAGAAGAGGATGA
37179_at	2762	TTCCAAGGTGTGTTCAAAGAGGCTT
37179_at	2763	GTCTAAGCTTTGGTCTATAAAGTGC
1486_at	2764	CAATGCCTGTTTATTCACCATCAAC
1486_at	2765	CAAAGAAGACCACACACTGGGAAAC
1486_at	2766	CACACTGGGAAACATCATTAAATCA
1486_at	2767	TAAATCACAACCTCCTAAAAGACCCG
1486_at	2768	GCAAGTGCTATTTGCTGGCTACAAA
1486_at	2769	GCACAAGATCATCATCCGAGTGCAG
1486_at	2770	GATCATCATCCGAGTGCAGACCACG
1486_at	2771	GGAAGCCTTTACCAACGCCATCACC
1486_at	2772	CATCAGTGAGCTGTCCCTGCTGGAG
1486_at	2773	TGAGCTGTCCCTGCTGGAGGAGCGC
1486_at	2774	GTCCCTGCTGGAGGAGCGCTTTCGG
1486_at	2775	GCTCGGCCTGTGAGCCCCGTTCTTA
1486_at	2776	CCTGTGAGCCCCGTTCTACCTGTG
1486_at	2777	GCTCCAGGTACCACACCGAGGAGAG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1486_at	2778	AGGAGAGCGGCCGGTCCCAGCCATG
1486_at	2779	GGTCCCAGCCATGGCCCGCCTTGTG
40182_s_at	2780	CACTCAAGAGTTAGAGCAGGTGGCT
40182_s_at	2781	CACTGCCGGCCACTTGGGGCAGACA
40182_s_at	2782	CTGCCGGCCACTTGGGGCAGACACA
40182_s_at	2783	GCCACTTGGGGCAGACACAGACACC
40182_s_at	2784	ACTTGGGGCAGACACAGACACCTCA
40182_s_at	2785	GGGGCAGACACAGACACCTCAAGGA
40182_s_at	2786	CTCAAGGATCTGTCACGGAAGGCGT
40182_s_at	2787	CTTGTAAGACGCTCCAGTCCCTACTA
40182_s_at	2788	TTGTAGACGCTCCAGTCCCTACTAC
40182_s_at	2789	TGTAGACGCTCCAGTCCCTACTACT
40182_s_at	2790	GTAAGACGCTCCAGTCCCTACTACTG
40182_s_at	2791	TAGACGCTCCAGTCCCTACTACTGT
40182_s_at	2792	GCTCCAGTCCCTACTACTGTGACGG
40182_s_at	2793	CCTACTACTGTGACGGCATTTCAT
40182_s_at	2794	TACTGTGACGGCATTTCATCCCTC
40182_s_at	2795	GGAAGGGACCTTGCAGGGACCTCTC
36419_at	2796	GATCAACTCCTTGATTACCATGTG
36419_at	2797	ATCAACTCCTTGATTACCATGTGG
36419_at	2798	ACTCCTTGATTACCATGTGGAGGA
36419_at	2799	CTTGATTACCATGTGGAGGATTAC
36419_at	2800	ATTTACCATGTGGAGGATTACAAC
36419_at	2801	AAAGCAGGCAGCTTGACTGCAGAGT
36419_at	2802	AGCAGGCAGCTTGACTGCAGAGTCT
36419_at	2803	GCAGGCAGCTTGACTGCAGAGTCTA
36419_at	2804	CAGCTTGACTGCAGAGTCTAATCAC
36419_at	2805	GCTTGACTGCAGAGTCTAATCACTG
36419_at	2806	GACTGCAGAGTCTAATCACTGCACT
36419_at	2807	CTGCAGAGTCTAATCACTGCACTGT
36419_at	2808	ATCACTGCACTGTTGCTTGTGGAAT
36419_at	2809	ACTGCACTGTTGCTTGTGGAATCTA
36419_at	2810	CTGCACTGTTGCTTGTGGAATCTAG
36419_at	2811	CACTGTTGCTTGTGGAATCTAGCAT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
32581_at	2812	GATCTTCGATCAGTTTTTATAGCAT
32581_at	2813	CAGTTTTTATAGCATCTATGGACAT
32581_at	2814	ATAGCATCTATGGACATAGAAAATC
32581_at	2815	TAGCATCTATGGACATAGAAAATCA
32581_at	2816	AAGACATTGTTACCATTTCGTCTTGC
32581_at	2817	GACATTGTTACCATTTCGTCTTGCAA
32581_at	2818	TCGTCTTGCAAATTTAAGACAACCTG
32581_at	2819	ATTTAAGACAACCTGAATGAAAAGCC
32581_at	2820	TTATTCTGTCATAGATAGTAAAGCC
32581_at	2821	ATTCTGTCATAGATAGTAAAGCCCC
32581_at	2822	CCATCTCAGTTTATTTAGTCCTGAG
32581_at	2823	TTTAGTCCTGAGGTTGGCAGCATGG
32581_at	2824	TACACAAAGAGATAACGCTGTTTCA
32581_at	2825	CGCTGTTTCATAATAAACAGGAATT
32581_at	2826	ATAGGTAAACCAGCATATCTACCTG
32581_at	2827	GCATATCTACCTGTATTTCTCAGAG
31308_at	2828	GCTCTCATGTCTAGTGATTATTACC
31308_at	2829	TTACCATTACTGCAGAACTCTGTGT
31308_at	2830	TGCCCACGGAGAACAGGCACAGCTG
31308_at	2831	GCCCACGGAGAACAGGCACAGCTGC
31308_at	2832	GACCGGCACGTCTCCTGCTTGGTCT
31308_at	2833	TCCTGCTTGGTCTCCTGTCTTGCTC
31308_at	2834	GCATTAACAGCCAACAATGCCTGAA
31308_at	2835	AGCGTAGCCTTCATGGAGAGTCCAC
31308_at	2836	GCCTTCATGGAGAGTCCACACGTCT
31308_at	2837	ATGGAGAGTCCACACGTCTAGGCAG
31308_at	2838	TAGGCAGGCCAGAGATTTGAGTTCT
31308_at	2839	ACCAGCCAATGAATAATGGTAATCA
31308_at	2840	TTCAAATAGCATTGTGCTTTATAGC
31308_at	2841	TAGCATTGTGCTTTATAGCACACAA
31308_at	2842	ACTGTGGAACGGTGCAGAGCCAGAA
31308_at	2843	GAGTTTGTGACTTTTCATCTTCAAA
36871_at	2844	TCCAGGCTGTACACTACAACGGTGT
36871_at	2845	GAGAACACCTTCCTTAGACTCACCG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36871_at	2846	TTAGCTGCTTTGCTCAGGAAGACAT
36871_at	2847	GCTTTGCTCAGGAAGACATTGCCAT
36871_at	2848	CTCAGGAAGACATTGCCATTTGTAG
36871_at	2849	ACCTTGCCATCAAGATGCCAGAGAA
36871_at	2850	TTGCCATCAAGATGCCAGAGAAAGC
36871_at	2851	AGTCAGCCTCCAGAACTCCCTAGAT
36871_at	2852	ATGCCCCCATGGAGGACTGTGTGAT
36871_at	2853	CCCATGGAGGACTGTGTGATCTCCA
36871_at	2854	CCATGGAGGACTGTGTGATCTCCAT
36871_at	2855	ACCATGTGTGCCAAGTTCCAGTTCA
36871_at	2856	CGCCAACACATGTGGGGCTCCAGAG
36871_at	2857	CACATGTGGGGCTCCAGAGACTCAC
36871_at	2858	TCCAGAGACTCACTGTGGAAGTGA
36871_at	2859	CAATCTAAACCAAACATGTGCTAGG
40956_at	2860	ACCTGTGCACATCTTGCTGGTGGAG
40956_at	2861	GGGGCTTTCGGCTCCCACACTGATG
40956_at	2862	TTCGGCTCCCACACTGATGATTCTC
40956_at	2863	CCCCAGCTCTCGTGTCTGGAGGAA
40956_at	2864	TGTCCTGGAGGAAGAGCTAGCTCCA
40956_at	2865	AGAGCTAGCTCCAGACATGGGTTGA
40956_at	2866	ATCACCTAGAGGAGCTCTGGCTAAG
40956_at	2867	CTAAGGCACAGTTTTCTAGAAATAA
40956_at	2868	CGAAGCTTAGCCTGTAGGTGCCAAG
40956_at	2869	CCTACTCTTGGCTGCGGCCACGTGA
40956_at	2870	AGCACTAGTGGACAAAGCCAGCAAA
40956_at	2871	TGGACAAAGCCAGCAAATGCGGCGT
40956_at	2872	GCAAATGCGGCGTTCCTGTGAGCAG
40956_at	2873	GCGGCGTTCCTGTGAGCAGATACCC
40956_at	2874	CTCAACCAGCCAGCTGTCAAAAGTA
40956_at	2875	CAGCCAGCTGTCAAAAGTATTTCAA
35151_at	2876	CCTAGTCAGAGAGTGCCTGGCAGAG
35151_at	2877	ATCCCGAGTTGCACTAACCATCCTG
35151_at	2878	TCCCGAGTTGCACTAACCATCCTGG
35151_at	2879	CGAGTTGCACTAACCATCCTGGGCT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35151_at	2880	GCACTAACCATCCTGGGCTTCCTGT
35151_at	2881	CTGGGCTTCCTGTCCTGTGTCCCTT
35151_at	2882	TTCCTGTCCTGTGTCCCTTGGTGGG
35151_at	2883	TCCAGGAACCAAGGAGTGGCCCTCC
35151_at	2884	AGGAACCAAGGAGTGGCCCTCCAGG
35151_at	2885	GTGGCCCTCCAGGTGGCAGCACTAA
35151_at	2886	CAGGTGGCAGCACTAAGGACACCCC
35151_at	2887	CCCCACAACAAGAGTTAGCAGCGAG
35151_at	2888	AGTTAGCAGCGAGGTCCCCATGAGT
35151_at	2889	TGTGTGTCTTTTGCTAAATATGCCC
35151_at	2890	GTGTGTCTTTTGCTAAATATGCCCT
35151_at	2891	GTGTCTTTTGCTAAATATGCCCTTT
39543_at	2892	GGTTGCCTTCTCATCCTCCAGGCAG
39543_at	2893	GTTGCCTTCTCATCCTCCAGGCAGT
39543_at	2894	TCTCCTTCCAATAAGGCCCGGTAGG
39543_at	2895	CGACTCGGCCACCAGCAGTGCGTAG
39543_at	2896	ACTCGGCCACCAGCAGTGCGTAGCT
39543_at	2897	TCGGCCACCAGCAGTGCGTAGCTGT
39543_at	2898	GGCCACCAGCAGTGCGTAGCTGTCTG
39543_at	2899	ACCAGCAGTGCGTAGCTGTCTGTGCA
39543_at	2900	CAGTGCGTAGCTGTCTGTGCACCTCC
39543_at	2901	AGCTCCCGCACGTCGCGTTCGTGGG
39543_at	2902	ACCTCCAGACTGAGGCCGGTCTTCA
39543_at	2903	ACTGAGGCCGGTCTTACCTGCAGG
39543_at	2904	TGAGGCCGGTCTTACCTGCAGGAG
39543_at	2905	AGGCCGGTCTTACCTGCAGGAGGT
39543_at	2906	GGCCGGTCTTACCTGCAGGAGGTC
39543_at	2907	TCTTACCTGCAGGAGGTCCTGATA
31454_f_at	2908	AGGGAGACTCCACATTGTTTCCATC
31454_f_at	2909	GGAGACTCCACATTGTTTCCATCTC
31454_f_at	2910	TTATCAAACCATGTAGAACAAACGG
31454_f_at	2911	TATCAAACCATGTAGAACAAACGGC
31454_f_at	2912	TCAAACCATGTAGAACAAACGGCTG
31454_f_at	2913	AAACCATGTAGAACAAACGGCTGTC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31454_f_at	2914	CCATGTAGAACAAACGGCTGTCTGC
31454_f_at	2915	CATGTAGAACAAACGGCTGTCTGCC
31454_f_at	2916	AGAACAAACGGCTGTCTGCCAACTG
31454_f_at	2917	GAACAAACGGCTGTCTGCCAACTGG
31454_f_at	2918	CAAACGGCTGTCTGCCAACTGGTAG
31454_f_at	2919	CGGCTGTCTGCCAACTGGTAGAGGC
31454_f_at	2920	GCTGTCTGCCAACTGGTAGAGGCAA
31454_f_at	2921	CTGTCTGCCAACTGGTAGAGGCAAA
31454_f_at	2922	GTCTGCCAACTGGTAGAGGCAAAGC
31454_f_at	2923	CTGCCAACTGGTAGAGGCAAAGCAG
40366_at	2924	CCACAGAAGCCAGGAGCAAATGTTT
40366_at	2925	GGAGCAAATGTTTCTGCAGTAGTCT
40366_at	2926	GTAGTCTCTGTGCTTTGACTCACCT
40366_at	2927	ACTGGAGCATCTGACTCACAAGAAG
40366_at	2928	CTCACAAGAAGACCAGACTGTGGAG
40366_at	2929	CAAGAAGACCAGACTGTGGAGAAAT
40366_at	2930	AATTCCTGTAGCATCTTCTGGAGTC
40366_at	2931	TCCTGTAGCATCTTCTGGAGTCTCC
40366_at	2932	TTCTGGAGTCTCCAGTGGTTGCTGT
40366_at	2933	AGTCTCCAGTGGTTGCTGTTGATGA
40366_at	2934	TTGCTGTTGATGAGGCCTCTTGGAC
40366_at	2935	GCCTCTTGGACCTCTGCTCTGAGGC
40366_at	2936	TTCCAGAGAGTCCTCTGGATGGCAC
40366_at	2937	GGCACCAGAGGCTGCAGAAGGCCAA
40366_at	2938	GCACCAGAGGCTGCAGAAGGCCAAG
40366_at	2939	AGCTAGAAGGCCACATGTCACCGTG
1251_g_at	2940	TCCAGGCCAAGAGTCTCAGCTGGCC
1251_g_at	2941	GGCCAAGAGTCTCAGCTGGCCGAGA
1251_g_at	2942	AAGAGTCTCAGCTGGCCGAGAGTCC
1251_g_at	2943	AGCTGGCCGAGAGTCCAGGCCTTGC
1251_g_at	2944	GCAGCCCGGCACAGCTGCTGGGAGC
1251_g_at	2945	CAGCTGCTGGGAGCCCTTGTGTGTC
1251_g_at	2946	TGGGAGCCCTTGTGTGTCTGGTCAC
1251_g_at	2947	AGCCCTTGTGTGTCTGGTCACACTT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1251_g_at	2948	TTGTGTGTCTGGTCACACTTTTTAG
1251_g_at	2949	GTGTCTGGTCACACTTTTTAGGCGT
1251_g_at	2950	CTGGTCACACTTTTTAGGCGTCACG
1251_g_at	2951	TTTTAGGCGTCACGCCAAAGGCCAG
1251_g_at	2952	GTCACGCCAAAGGCCAGCCTCCTGG
1251_g_at	2953	CCAATACCCATTTTGAAGCCCCTG
1251_g_at	2954	TTGGAAGCCCCTGTGGCCGTGTGGA
1251_g_at	2955	AGCCCCTGTGGCCGTGTGGATGTCTG
115_at	2956	ACTGTGATCCTGGACTCGCTGTAGG
115_at	2957	TCATCAACACCGAAAGGGACGATGA
115_at	2958	ACACCGAAAGGGACGATGACTATGC
115_at	2959	TCACCCAGTCCTACTGGGACACCAA
115_at	2960	CTCAGGGATACTCGGGCCTTTCTGT
115_at	2961	GATACTCGGGCCTTTCTGTGAAAGT
115_at	2962	TTGTAAACTCCACCACAGGGCCTGG
115_at	2963	GCACCCTGTGGCATGACCCTCGTCA
115_at	2964	CTCGTCACATAGGCTGGAAAGATTT
115_at	2965	AAGATTTACACCGCCTACAGATGGCG
115_at	2966	GTCTCAGCCACAGGCCAAAGACGGG
115_at	2967	GCCACAGGCCAAAGACGGGTTCAT
115_at	2968	AGACGGGTTCATTAGAGTGGTGAT
115_at	2969	AAACCTATGCTGGTGGTAGACTAGG
115_at	2970	ATGCTGGTGGTAGACTAGGGTTGTT
115_at	2971	TGGTGTCTCTCTGACCTGAAATA
34447_at	2972	CCCTGCAGGCGGTATCCAGAGGTGA
34447_at	2973	GCCTGAAATGTTTCCAGGCATGACC
34447_at	2974	TTTCCAGGCATGACCCTGGAGCCCG
34447_at	2975	CCCTGCCTGTGAGTGACATCGGTTC
34447_at	2976	CATCGGTTCAGGAGGAGACAGTCAG
34447_at	2977	TTCAGGAGGAGACAGTCAGGAAGCC
34447_at	2978	AGACAGTCAGGAAGCCTCCTGCTGA
34447_at	2979	CTCCTGCTGAGTGGTCCACATTCTG
34447_at	2980	CTGAGTGGTCCACATTCTGCTGCCC
34447_at	2981	TGAGTGGTCCACATTCTGCTGCCCC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34447_at	2982	TTGGGCTCTGCGTCCCACTGAGTCT
34447_at	2983	TGAGTCTCATTCCCTCTGTCCCCGAG
34447_at	2984	AGCCGAGCTCTCCTGGGCCAGGGTC
34447_at	2985	CTCTCCTGGGCCAGGGTCTCGTCAG
34447_at	2986	AATTGAGGTTAGGAACCCGGCATGC
34447_at	2987	ATTGAGGTTAGGAACCCGGCATGCC
38879_at	2988	AGGGGCATTTTGACACCCTCTCTAA
38879_at	2989	TGACACCCTCTCTAAGGGTGAGCTG
38879_at	2990	CAGCTGCTTACAAAGGAGCTTGCAA
38879_at	2991	TGCTTACAAAGGAGCTTGCAAACAC
38879_at	2992	GAGCTTGCAAACACCATCAAGAATA
38879_at	2993	AAAGCTGTCATTGATGAAATATTCC
38879_at	2994	TCCAAGGCCTGGATGCTAATCAAGA
38879_at	2995	ATGCTAATCAAGATGAACAGGTCGA
38879_at	2996	ATGAACAGGTCGACTTTCAAGAATT
38879_at	2997	AGGTCGACTTTCAAGAATTCATATC
38879_at	2998	CCCTGGTAGCCATTGCGCTGAAGGC
38879_at	2999	TAGCCATTGCGCTGAAGGCTGCCCA
38879_at	3000	CTGTAGCTCCACATTCCTGTGCATT
38879_at	3001	CTCCACATTCCTGTGCATTGAGGGG
38879_at	3002	ATTCCTGTGCATTGAGGGGGTTAACA
38879_at	3003	TCCTGTGCATTGAGGGGGTTAACATT
39389_at	3004	TATATTAAGCAGAAATCCTGCAATG
39389_at	3005	ATTAAGCAGAAATCCTGCAATGAAA
39389_at	3006	TTAAGCAGAAATCCTGCAATGAAAG
39389_at	3007	AATCCTGCAATGAAAGGTACTATAT
39389_at	3008	GTA CTATATTTGCTAGACTCTAGAC
39389_at	3009	CTATATTTGCTAGACTCTAGACAAG
39389_at	3010	TATATTTGCTAGACTCTAGACAAGA
39389_at	3011	TTTGCTAGACTCTAGACAAGATATT
39389_at	3012	GCTAGACTCTAGACAAGATATTGTA
39389_at	3013	TCTTCAGTATGATCTTGTGCTGTGC
39389_at	3014	GTATGATCTTGTGCTGTGCTATCCG
39389_at	3015	ATGATCTTGTGCTGTGCTATCCGCA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39389_at	3016	TTTAGTATTCATTCTGCATTGCTAG
39389_at	3017	GTATTCATTCTGCATTGCTAGATAA
39389_at	3018	TTCATTCTGCATTGCTAGATAAAAG
39389_at	3019	ATTCTGCATTGCTAGATAAAAGCTG
39729_at	3020	CCAGCCGCACACAGGCCTAGAGGTA
39729_at	3021	CGCACACAGGCCTAGAGGTAACCAA
39729_at	3022	GCACACAGGCCTAGAGGTAACCAAT
39729_at	3023	CACAGGCCTAGAGGTAACCAATAAA
39729_at	3024	ACAGGCCTAGAGGTAACCAATAAAG
39729_at	3025	CAGGCCTAGAGGTAACCAATAAAGT
39729_at	3026	ACACAATTAGGCTGGCTAACGGATA
39729_at	3027	TTAGGCTGGCTAACGGATAGTGAGC
39729_at	3028	GCTGGCTAACGGATAGTGAGCTTGT
39729_at	3029	CTGGCTAACGGATAGTGAGCTTGTG
39729_at	3030	GCTAACGGATAGTGAGCTTGTGCCC
39729_at	3031	TAACGGATAGTGAGCTTGTGCCCCT
39729_at	3032	TCCAAACTCCACAGTATGGGACCCT
39729_at	3033	CCAAACTCCACAGTATGGGACCCTG
39729_at	3034	CAAACCTCCACAGTATGGGACCCTGG
39729_at	3035	AACTCCACAGTATGGGACCCTGGAG
39448_r_at	3036	GAGCCAGAGCAGGTGGGTGAGGTAG
39448_r_at	3037	AGAGCAGGTGGGTGAGGTAGTTGAG
39448_r_at	3038	CTTCATCATGTCCTCCGTGAGGGGG
39448_r_at	3039	ATCATGTCCTCCGTGAGGGGGGTGG
39448_r_at	3040	CCTCCGTGAGGGGGGTGGGCAGCCA
39448_r_at	3041	CGTGAGGGGGGTGGGCAGCCATTCC
39448_r_at	3042	TCCTCAAGGGAACCTTTCCCCCTCT
39448_r_at	3043	TTCTTGTAGTCCTCCCCCTCCTCT
39448_r_at	3044	CCCTCCTCTGTCTCCTTCTTCGGCC
39448_r_at	3045	CTCCTCTGTCTCCTTCTTCGGCCTC
39448_r_at	3046	CCTCTGTCTCCTTCTTCGGCCTCTT
39448_r_at	3047	TCTGTCTCCTTCTTCGGCCTCTTCT
39448_r_at	3048	TCTCCTTCTTCGGCCTCTTCTTCT
39448_r_at	3049	GCCTCTTCTTTCTCAAGAATCATCC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39448_r_at	3050	AAAAC TAGCAATCTGCAGGTAGGGC
39448_r_at	3051	TCAAGAGTCTTCCTTAGATCAACTT
33759_at	3052	AGCTTTCTTGCTAGCCCCCTAGTCG
33759_at	3053	CACCAAAC TAGTAAC TAGTGGGGCT
33759_at	3054	ATCATTATTGAGTCACCATTGACAG
33759_at	3055	CATTGACAGGCACTATTCTAATCAG
33759_at	3056	CAGGCACTATTCTAATCAGTAGTTC
33759_at	3057	AGGCACTATTCTAATCAGTAGTTCA
33759_at	3058	TACTAGTCTTTTCCTCTAGGAAAAG
33759_at	3059	TTCTCTAGGAAAAGGGATACTTTG
33759_at	3060	GGCCAGAGGCCCATTAGTTGAGAAA
33759_at	3061	GAGGCCCATTAGTTGAGAAAGTCAC
33759_at	3062	AGGCCCATTAGTTGAGAAAGTCACA
33759_at	3063	GAAATGACAACAAGGCCCTTTAACT
33759_at	3064	AACTTGTCTTCTAGTTTAGAGACAT
33759_at	3065	GAGACATCCTTCATTTGACATTTAG
33759_at	3066	CATTTAGTAGAATTCCTCTTTGGCC
33759_at	3067	AACTATGGCTGTTGAGGTTCTCATT
33449_at	3068	GTGTATCTTTAGGTGCAATCACAGC
33449_at	3069	GTGCAATCACAGCAGTCCTCTCATC
33449_at	3070	CAACCCTGAGCCACCGTAATTGAGC
33449_at	3071	AGCTTTCCTTTCTGTTCCCTGTGGC
33449_at	3072	GCTAAGACAGTAAGCCAGTGTGAGA
33449_at	3073	TCCTCCCTTGGGAAGTCAGAGCTGC
33449_at	3074	GAAGTCAGAGCTGCTGCCCTGGGTC
33449_at	3075	GAGCTGCTGCCCTGGGTCCTGCAGA
33449_at	3076	TGCAGAGAAACCTGGCCTTCAGCAG
33449_at	3077	TGGCCTTCAGCAGACCTGTTTCTCT
33449_at	3078	TGACTTCCGTTTGCTTTTAGACCTT
33449_at	3079	GTTTGCTTTTAGACCTTCATTCTAG
33449_at	3080	CTAGTCCCCTAATGAATGTATAATG
33449_at	3081	GTGTAGGCCTTTCCATTCCATTAT
33449_at	3082	CTGAGTGTCTACAATAAACTTCCG
33449_at	3083	GAGTGTCCTACAATAAACTTCCGTA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31812_at	3084	GAGCTCAGCAGGAGGGCAACATTCA
31812_at	3085	GGGCAACATTCATCCGGGTGACCCA
31812_at	3086	AGTGGAAGCGTCCAAACCTGCTTTT
31812_at	3087	GAAGCGTCCAAACCTGCTTTTCCCA
31812_at	3088	GCTTCTGGCTGCTCCTGAATGGTGG
31812_at	3089	CTTCTGGCTGCTCCTGAATGGTGGGA
31812_at	3090	GCTGCTCCTGAATGGTGGGAATGCTG
31812_at	3091	GCTGTGTCCTCTCTTCTGTCTCCTG
31812_at	3092	GGGCCCAGACGCAAGGCACCGATTG
31812_at	3093	GCAAGGCACCGATTGGGCCAACATC
31812_at	3094	TGGGCCAACATCAGAGCCCTGCTGC
31812_at	3095	TTGTTTTGCTACCTTCCTAGACAGG
31812_at	3096	TAGACAGGCTGATGGCAAGCCTCTC
31812_at	3097	CTCTCCCGGCGATTAGCAGACAAGT
31812_at	3098	TAGCAGACAAGTCACCTTAGGAGGG
31812_at	3099	TGGACAGGCCGAGTCAAAGTAACT
40578_s_at	3100	GCTGCTGACCTTACGCCTGTATATT
40578_s_at	3101	TGACCTTACGCCTGTATATTAAGCC
40578_s_at	3102	GACCTTACGCCTGTATATTAAGCCT
40578_s_at	3103	ACATCATGTGCGTCTCTTGGGATCC
40578_s_at	3104	TCTTGGGATCCAGCAAAAGTGTTAA
40578_s_at	3105	GGATCCAGCAAAAGTGTTAAGCCAC
40578_s_at	3106	AAGTGTTAAGCCACAATGCCCTTGT
40578_s_at	3107	GTTAAGCCACAATGCCCTTGTGCCT
40578_s_at	3108	GCCACAATGCCCTTGTGCCTTTTAA
40578_s_at	3109	GTGATTTTCAGCAAATCTCATGATAA
40578_s_at	3110	GATTTTCAGCAAATCTCATGATAAAG
40578_s_at	3111	AAATCTCATGATAAAGGACAAGGTC
40578_s_at	3112	GACAAGGTCAAGAACTCCAGAGCAC
40578_s_at	3113	ACAAGGTCAAGAACTCCAGAGCACT
40578_s_at	3114	GGTCAAGAACTCCAGAGCACTGAGC
40578_s_at	3115	AACTCCAGAGCACTGAGCAGAGAGG
40766_at	3116	CTTTCCGCCTCTTTGAGACCAAGAT
40766_at	3117	TTTCCGCCTCTTTGAGACCAAGATC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40766_at	3118	TTCCGCCTCTTTGAGACCAAGATCA
40766_at	3119	TCCGCCTCTTTGAGACCAAGATCAC
40766_at	3120	GCCTCTTTGAGACCAAGATCACCCA
40766_at	3121	GAGACCAAGATCACCCAAGTCCTGC
40766_at	3122	TTCGCTTGGAACCTGGGAAAGAATA
40766_at	3123	TCGCTTGGAACCTGGGAAAGAATAT
40766_at	3124	CTCGAATAGCTGGATCGAGGAGATG
40766_at	3125	TAGCTGGATCGAGGAGATGCCCTCT
40766_at	3126	GAGGAGATGCCCTCTGAACGCCTGT
40766_at	3127	AGGAGATGCCCTCTGAACGCCTGTG
40766_at	3128	GAGATGCCCTCTGAACGCCTGTGCC
40766_at	3129	AGATGCCCTCTGAACGCCTGTGCCG
40766_at	3130	GATGCCCTCTGAACGCCTGTGCCGG
40766_at	3131	CTTCCTCCAGGAGTATGGCACTCAG
31320_at	3132	CAGAGAGCGCGCTCGCCCAGTGATG
31320_at	3133	GTGATGTGTAGCACCCCTTGCACCCA
31320_at	3134	TGTAGCACCCCTTGCACCCAGGAGGA
31320_at	3135	ATGCTCTGGGGGACCTCCATCTGCC
31320_at	3136	CCGTCATGGGCTGGAACCTGCCTCCG
31320_at	3137	GCTGGAACCTGCCTCCGAGACGAGTC
31320_at	3138	GACGAGTCCACCTGCAGCGTGGTCA
31320_at	3139	GTCGCACTATGTGACCACCCGGAAA
31320_at	3140	TCCACCCTGGCTATCATCTGGGGA
31320_at	3141	TCCTGGGGACGTTTGCTGCTTGCTG
31320_at	3142	GGACGTTTGCTGCTTGCTGGATGCC
31320_at	3143	CCTTGATAGCGGATTACACCTACCC
31320_at	3144	GTCATATATGCTTTCAGAAACCAAG
31320_at	3145	GAAACCAAGAGATCCAGAAAGCGCT
31320_at	3146	TCCAGAAAGCGCTCTGTCTCATTTG
31320_at	3147	TTGCTGCGGCTGCATCCCGTCCAGT
34378_at	3148	ATCCTCAGCTGACTGAGTCTCAGAA
34378_at	3149	CTGAGTCTCAGAATGCTCAGGACCA
34378_at	3150	CTCAGAATGCTCAGGACCAAGGTGC
34378_at	3151	ATGCTCAGGACCAAGGTGCAGAGAT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
34378_at	3152	GCCAGGAGACCCAGCGATCTGAGCA
34378_at	3153	CCTATCACTAGTGCATGCTGTGGCC
34378_at	3154	GCTGTGGCCAGACAGATGACACCTT
34378_at	3155	CAGATGACACCTTTTGTATGTTGA
34378_at	3156	TGAAATTAACCTTGCTAGGCAACCCT
34378_at	3157	ACTTGCTAGGCAACCCTAAATTGGG
34378_at	3158	GCTAGGCAACCCTAAATTGGGAAGC
34378_at	3159	TGTCTGCTCTGGTGTGATCTGAAAA
34378_at	3160	CTCTGGTGTGATCTGAAAAGGCGTC
34378_at	3161	CTGAAAAGGCGTCTTCACTGCTTTA
34378_at	3162	AGGCGTCTTCACTGCTTTATCTCAT
34378_at	3163	CACTGCTTTATCTCATGATGCTTGC
40773_at	3164	CAAGCAGGAGCTTAAGATGGGCAAG
40773_at	3165	TAAGATGGGCAAGACCTGGGGCCCT
40773_at	3166	GGGCCCTGGGCAGACGCATCAAAGC
40773_at	3167	CTGGGCAGACGCATCAAAGCAGGCA
40773_at	3168	TCAAAGCAGGCAGAAGCAGGCATGG
40773_at	3169	CAGAAGCAGGCATGGCCAGCAGGAA
40773_at	3170	CCCTGGGCAAGACCAACGTCAAGGA
40773_at	3171	TGGGCAAGACCAACGTCAAGGACGA
40773_at	3172	GTACCGACGCCGAGGAGACCATTCT
40773_at	3173	CGACGCCGAGGAGACCATTCTTAAC
40773_at	3174	TCTTAACGCCTTCAAGATGCTGGAC
40773_at	3175	TCAAGATGCTGGACCCGGACGGGAA
40773_at	3176	AAATCAACAAGGAGTACATCAAGCG
40773_at	3177	AGGAGTACATCAAGCGTCTGCTGAT
40773_at	3178	GATGTCCCAGGCTGACAAGATGACG
40773_at	3179	CCAGGCTGACAAGATGACGGCGGAA
38726_at	3180	GCAGAGTCCCCATGGCATGGAGCTT
38726_at	3181	AGTCCCCATGGCATGGAGCTTACAC
38726_at	3182	GCATGGAGCTTACACCTGACTGACT
38726_at	3183	ATGGAGCTTACACCTGACTGACTGG
38726_at	3184	TGGAGCTTACACCTGACTGACTGGA
38726_at	3185	GGAGCTTACACCTGACTGACTGGAG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38726_at	3186	GAGCTTACACCTGACTGACTGGAGC
38726_at	3187	GCTTACACCTGACTGACTGGAGCCC
38726_at	3188	CCCACAAAGCCTTCTGGACCTGGAA
38726_at	3189	CACAAAGCCTTCTGGACCTGGAAAG
38726_at	3190	CAAAGCCTTCTGGACCTGGAAAGCC
38726_at	3191	AAAGCCTTCTGGACCTGGAAAGCCT
38726_at	3192	AAGCCTTCTGGACCTGGAAAGCCTG
38726_at	3193	CTTCTGGACCTGGAAAGCCTGGGGA
38726_at	3194	TTCTGGACCTGGAAAGCCTGGGGAA
38726_at	3195	GGAAGGACTGACAGACCCCAGGACC
1832_at	3196	CATAATTGCTGTTCTGCTGAATCAA
1832_at	3197	TGCTGTTCTGCTGAATCAAATCTCT
1832_at	3198	TCTGCTGAATCAAATCTCTTCCACA
1832_at	3199	GAATCAAATCTCTTCCACATGGGTG
1832_at	3200	ATGGGTGCATTTGTAGCTCTGGACC
1832_at	3201	GCATTTGTAGCTCTGGACCTGTCTC
1832_at	3202	GTAGCTCTGGACCTGTCTCTACCTA
1832_at	3203	AAGACACTGAGGAGATACTGAACAT
1832_at	3204	TTCAAGACTTAGCTCCTGTTGTCAT
1832_at	3205	TTGCCCCCAGATACATGGTGATGGT
1832_at	3206	CCAGATACATGGTGATGGTTAGCAT
1832_at	3207	CTCTCAGTTCTACACTGATACACTT
1832_at	3208	GTTCTACACTGATACACTTGAAGGA
1832_at	3209	CACTGATACACTTGAAGGACCATT
1832_at	3210	CATTGCCATAGCTGACTACAAATTA
1832_at	3211	GTTTCTGCATAGAGTCTTTATGTCC
36543_at	3212	GGGTGCATTTCTAGGACTTTTCTAA
36543_at	3213	GTGCATTTCTAGGACTTTTCTAACA
36543_at	3214	ATCTGCACTTTAACTGACTTAAGTG
36543_at	3215	CTGCACTTTAACTGACTTAAGTGGC
36543_at	3216	GCACTTTAACTGACTTAAGTGGCAT
36543_at	3217	CACTTTAACTGACTTAAGTGGCATT
36543_at	3218	ACTTTAACTGACTTAAGTGGCATT
36543_at	3219	CTTTAACTGACTTAAGTGGCATTAA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36543_at	3220	TTAACTGACTTAAGTGGCATTAAAC
36543_at	3221	TAACTGACTTAAGTGGCATTAAACA
36543_at	3222	AACTGACTTAAGTGGCATTAAACAT
36543_at	3223	GGTACTTAAAGCTTCTATGGTTGAC
36543_at	3224	GTACTTAAAGCTTCTATGGTTGACA
36543_at	3225	TACTTAAAGCTTCTATGGTTGACAT
36543_at	3226	ACTTAAAGCTTCTATGGTTGACATT
36543_at	3227	CTTAAAGCTTCTATGGTTGACATTG
137_at	3228	CCTGGCACTTGGACTCTCCTAGTGA
137_at	3229	AGCCTGTTTGGTGGTCTCTTCACAC
137_at	3230	TTTGGTGGTCTCTTCACACGGACGC
137_at	3231	TTCACACGGACGCGCGTGACACAAT
137_at	3232	CGGACGCGCGTGACACAATGCTGGG
137_at	3233	CAAATATCAAACACGGACCCATAGA
137_at	3234	CCGACAAGCCTTCAGCCACAGGGGA
137_at	3235	CAGCCACAGGGGAGCCACACAGAGA
137_at	3236	CAGGGGAGCCACACAGAGATGTCCA
137_at	3237	AGCCACACAGAGATGTCCAAACTGT
137_at	3238	ATGTCCAAACTGTCGTGCAAACCCA
137_at	3239	AAACTGTCGTGCAAACCCAGTGAGA
137_at	3240	GGACTCAGTGGACACTCAGACCAGC
137_at	3241	GACCAGCTCCCAGATGGCCCTGGAC
137_at	3242	GAAGGTCCCTTATTGTGGCTGATAT
137_at	3243	CTGATATTAAGTGTCAATGGTTATG
38585_at	3244	CCATAAAGCACCTGGATGATCTCAA
38585_at	3245	AGCACCTGGATGATCTCAAGGGCAC
38585_at	3246	CTCCTGGGAAATGTGCTGGTGACCG
38585_at	3247	TGGTGACCGTTTTGGCAATCCATTT
38585_at	3248	CCGTTTTGGCAATCCATTTTCGGCAA
38585_at	3249	GTTTTGGCAATCCATTTTCGGCAAAG
38585_at	3250	TGGCAATCCATTTTCGGCAAAGAATT
38585_at	3251	TTCGGCAAAGAATTACCCCTGAGG
38585_at	3252	CTCCTAGTCCAGACGCCATGGGTCA
38585_at	3253	GTCCAGACGCCATGGGTCAATTCAC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38585_at	3254	ACGCCATGGGTCATTTCACAGAGGA
38585_at	3255	ATTTCACAGAGGAGGACAAGGCTAC
38585_at	3256	AGGACAAGGCTACTATCACAAGCCT
38585_at	3257	AGGCTACTATCACAAGCCTGTGGGG
38585_at	3258	CTATCACAAGCCTGTGGGGCAAGGT
38585_at	3259	ATCACAAGCCTGTGGGGCAAGGTGA
34022_at	3260	GTATCATTGACACTTCCTGCAGGGT
34022_at	3261	TGACACTTCCTGCAGGGTGGTCCCT
34022_at	3262	CAGCAGCTTTCTAGGGACAGCTGGA
34022_at	3263	TGACTATTTCTTACGAGGGTTCTAC
34022_at	3264	TCTTACGAGGGTTCTACTTATTTAT
34022_at	3265	CTTACGAGGGTTCTACTTATTTATG
34022_at	3266	TGTGTTTCATCAAACATAGCTCAGT
34022_at	3267	GTGTTTCATCAAACATAGCTCAGTC
34022_at	3268	GTCAGCCACCTTGATAAATGACAGG
34022_at	3269	TCAGCCACCTTGATAAATGACAGGG
34022_at	3270	AGCCACCTTGATAAATGACAGGGTG
34022_at	3271	ATTTTTATGCTGAAGTTTCCCTTAG
34022_at	3272	TTATGCTGAAGTTTCCCTTAGACAT
34022_at	3273	TATGCTGAAGTTTCCCTTAGACATT
34022_at	3274	TTAATGTCCATTCTGCAGCGTTTCT
34022_at	3275	TAATGTCCATTCTGCAGCGTTTCTC
38021_at	3276	TGTCTGATCTGTGCTTTCCAGCTCA
38021_at	3277	TCTGATCTGTGCTTTCCAGCTCACC
38021_at	3278	CCTCTGTTCCCCTAGTAAGTGCCTT
38021_at	3279	CTCTGTTCCCCTAGTAAGTGCCTTC
38021_at	3280	TCCCCTAGTAAGTGCCTTCCATGTC
38021_at	3281	AGTGCCTTCCATGTGCGCCTCTAAC
38021_at	3282	TTGGGCCCAGGGACACCAGCCAGGC
38021_at	3283	GGGACACCAGCCAGGCTCTGTGCTG
38021_at	3284	AGGCTCTGTGCTGACCCTCCTGTTG
38021_at	3285	GGCTCTGTGCTGACCCTCCTGTTGC
38021_at	3286	GAGCTTTGCATGTTCCACTAACCCC
38021_at	3287	AGCTTTGCATGTTCCACTAACCCCG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38021_at	3288	TGCATGTTCCACTAACCCCGGGCGG
38021_at	3289	TGGCGCCTCTGCAAGGGCAGAACAC
38021_at	3290	TCTGCAAGGGCAGAACACTAACCTG
38021_at	3291	CAGAACACTAACCTGACCGTGGGCG
33143_s_at	3292	ATTTTACAAACTGGACTGGCTCAGG
33143_s_at	3293	TACAAACTGGACTGGCTCAGGCAGG
33143_s_at	3294	TATGCTCAAGGACCTGGAAACCCAT
33143_s_at	3295	TGCTCAAGGACCTGGAAACCCATGC
33143_s_at	3296	CAAGGACCTGGAAACCCATGCTTCG
33143_s_at	3297	CTGGAAACCCATGCTTCGAGACAAC
33143_s_at	3298	TGGAAACCCATGCTTCGAGACAACG
33143_s_at	3299	AACCCATGCTTCGAGACAACGTGAC
33143_s_at	3300	CCCATGCTTCGAGACAACGTGACTT
33143_s_at	3301	TGCTTCGAGACAACGTGACTTTAAT
33143_s_at	3302	TCGAGACAACGTGACTTTAATGGGA
33143_s_at	3303	ACCCCTCTTGAGTGTCTTGGGGACA
33143_s_at	3304	CCCCTCTTGAGTGTCTTGGGGACAG
33143_s_at	3305	TCTTGAGTGTCTTGGGGACAGCTCT
33143_s_at	3306	AGTGTCTTGGGGACAGCTCTTTCCA
33143_s_at	3307	GTGTCTTGGGGACAGCTCTTTCCAC
37758_s_at	3308	GAAAGTTGCATTCTGCTGTTTGCTT
37758_s_at	3309	AAAGTTGCATTCTGCTGTTTGCTTG
37758_s_at	3310	AAGTTGCATTCTGCTGTTTGCTTGG
37758_s_at	3311	GTTGCATTCTGCTGTTTGCTTGGAC
37758_s_at	3312	TTGCATTCTGCTGTTTGCTTGGACA
37758_s_at	3313	TGCATTCTGCTGTTTGCTTGGACAC
37758_s_at	3314	CATTCTGCTGTTTGCTTGGACACCG
37758_s_at	3315	ATTCTGCTGTTTGCTTGGACACCGT
37758_s_at	3316	TTCTGCTGTTTGCTTGGACACCGTA
37758_s_at	3317	TCTGCTGTTTGCTTGGACACCGTAC
37758_s_at	3318	TGCTGTTTGCTTGGACACCGTACCA
37758_s_at	3319	GCTGTTTGCTTGGACACCGTACCAC
37758_s_at	3320	CTGTTTGCTTGGACACCGTACCACT
37758_s_at	3321	GTTTGCTTGGACACCGTACCACTGA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37758_s_at	3322	GCTTGGACACCGTACCACTGAACAA
37758_s_at	3323	CTTGGACACCGTACCACTGAACAAA
40850_at	3324	AGACCGCCTTGTACCGGAAAATGCT
40850_at	3325	GCAAGGGTGCCTGGTCCATCCCATG
40850_at	3326	GTGCCTGGTCCATCCCATGGAAGTG
40850_at	3327	CCATCCCATGGAAGTGGCTGTTTGG
40850_at	3328	TGTTTGGGGCGACTGCTGTTGCCTT
40850_at	3329	ACTGAGGCCCTCTAGGAGGAAAGCC
40850_at	3330	CTGAGGCCCTCTAGGAGGAAAGCCC
40850_at	3331	GAGGCCCTCTAGGAGGAAAGCCCAG
40850_at	3332	AGGCCCTCTAGGAGGAAAGCCCAGA
40850_at	3333	GGCCCTCTAGGAGGAAAGCCCAGAG
40850_at	3334	GCCCTCTAGGAGGAAAGCCCAGAGG
40850_at	3335	CCTCTAGGAGGAAAGCCCAGAGGGA
40850_at	3336	TAGGTCTCCGCCAGGGCTGGCCTCA
40850_at	3337	AGGGCTGGCCTCAGTTTCTCCTCAA
40850_at	3338	GGCTGGCCTCAGTTTCTCCTCAACA
40850_at	3339	AGTTTCTCCTCAACAGGCCTGGGGG
36766_at	3340	TACCTGGGCTCAATGGTTTGAAACC
36766_at	3341	CCTGGGCTCAATGGTTTGAAACCCA
36766_at	3342	CTCAATGGTTTGAAACCCAGCACAT
36766_at	3343	GGTTTGAAACCCAGCACATCAATAT
36766_at	3344	GTTTGAAACCCAGCACATCAATATG
36766_at	3345	ATGACCTCCCAGCAATGCACCAATG
36766_at	3346	CTCCCAGCAATGCACCAATGCAATG
36766_at	3347	GCCAAGCTCCTCAATCATAGCCAAG
36766_at	3348	TCTCTCCATATACTTTGGGTATCAG
36766_at	3349	CTCCATATACTTTGGGTATCAGCAT
36766_at	3350	ATATACTTTGGGTATCAGCATCTGT
36766_at	3351	ATACTTTGGGTATCAGCATCTGTCC
36766_at	3352	TACTTTGGGTATCAGCATCTGTCCT
36766_at	3353	ACTTTGGGTATCAGCATCTGTCCTC
36766_at	3354	TTTGGGTATCAGCATCTGTCCTCAT
36766_at	3355	GGTATCAGCATCTGTCCTCATCAGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38201_at	3356	GAGACAATACACATTCCAACATATGG
38201_at	3357	TGGAGAATGGTCCTAAGCTGGCAAG
38201_at	3358	ATGGTCCTAAGCTGGCAAGCCGCAT
38201_at	3359	TGGCAAGCCGCATCTTGAGCAAATT
38201_at	3360	CAAATTAACATGATATCCAGTATGGA
38201_at	3361	ATTGTGATAGATTTCTTTGGCTACC
38201_at	3362	CTACCTGTGCATAATGTAGTTTGTA
38201_at	3363	AGAGTGATTGTTTCTTCATGCCAGA
38201_at	3364	TCATAACTTGGTAGTAGTAACTTAC
38201_at	3365	GTAAGCCATATAACATGGGATTTTC
38201_at	3366	TAGATGGCATCATTCTTCCAGGAGT
38201_at	3367	GCATCATTCTTCCAGGAGTGACAAG
38201_at	3368	TGACAAGGCGGTGCATTCTGGACCT
38201_at	3369	GGCGGTGCATTCTGGACCTGGCACA
38201_at	3370	TCTGGACCTGGCACATCAGTGGGTG
38201_at	3371	GAACAACTTTTGTAAGCCTGAAATA
40847_at	3372	CCCAGTTCATTTTCAGCCTTCCAGTG
40847_at	3373	TTCCAGTGCTACACCCACTTCTTGG
40847_at	3374	AGTGCTACACCCACTTCTTGGCTGA
40847_at	3375	TGCTACACCCACTTCTTGGCTGACA
40847_at	3376	CCACTTCTTGGCTGACACACTTCTG
40847_at	3377	CACTTCTTGGCTGACACACTTCTGC
40847_at	3378	ACTTCTTGGCTGACACACTTCTGCT
40847_at	3379	CTTCTTGGCTGACACACTTCTGCTC
40847_at	3380	TTCTTGGCTGACACACTTCTGCTCT
40847_at	3381	TCTTGGCTGACACACTTCTGCTCTA
40847_at	3382	CTTGGCTGACACACTTCTGCTCTAA
40847_at	3383	TTGGCTGACACACTTCTGCTCTAAG
40847_at	3384	GGCTGACACACTTCTGCTCTAAGAG
40847_at	3385	CTGACACACTTCTGCTCTAAGAGTC
40847_at	3386	TGACACACTTCTGCTCTAAGAGTCT
40847_at	3387	GACACACTTCTGCTCTAAGAGTCTC
36036_at	3388	GCAGAGCAGGCTACGTCCTCACTGA
36036_at	3389	CAGAGCAGGCTACGTCCTCACTGAG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36036_at	3390	AGAGCAGGCTACGTCCTCACTGAGG
36036_at	3391	GAGCAGGCTACGTCCTCACTGAGGT
36036_at	3392	AGCAGGCTACGTCCTCACTGAGGTG
36036_at	3393	CAGGCTACGTCCTCACTGAGGTGTT
36036_at	3394	GGCTACGTCCTCACTGAGGTGTTCT
36036_at	3395	CTACGTCCTCACTGAGGTGTTCTTC
36036_at	3396	ACGTCCTCACTGAGGTGTTCTTCAT
36036_at	3397	TCACTGAGGTGTTCTTCATGAGAGT
36036_at	3398	TGTTCTTCATGAGAGTACTAGCCTC
36036_at	3399	GTTCTTCATGAGAGTACTAGCCTCC
36036_at	3400	TCCCCACAGCGCAGAGGAAACAGGC
36036_at	3401	CCCACAGCGCAGAGGAAACAGGCCA
36036_at	3402	CACAGCGCAGAGGAAACAGGCCAGC
36036_at	3403	CCAGCCCAGTGACATGACGTTATTA
2092_s_at	3404	TGCATCTTCTGAGGTCAATTA AAAAG
2092_s_at	3405	ACAATTTCTCACTTTGCATTTAGTC
2092_s_at	3406	CATGAAATGCTTCTTTCTCAGTTTA
2092_s_at	3407	ATAATTAGTTTAGTTTGTGGCTTCA
2092_s_at	3408	TAGTTTGTGGCTTCATGGAAACTCC
2092_s_at	3409	AAGCTTCAGGGTTATGTCTATGTTT
2092_s_at	3410	AGAGCAATGAGCATTCCGATGTGAT
2092_s_at	3411	AGCATTCCGATGTGATTGATAGTCA
2092_s_at	3412	TCAGGAACTTTCCAAAGTCAGCCGT
2092_s_at	3413	AGCCGTGAATTCCACAGCCATGAAT
2092_s_at	3414	ATTCCACAGCCATGAATTTACAGC
2092_s_at	3415	CCATGAATTTACAGCCATGAAGAT
2092_s_at	3416	ACAGCCATGAAGATATGCTGGTTGT
2092_s_at	3417	ATGCTGGTTGTAGACCCCAAAGTA
2092_s_at	3418	ACCTGAAATTTTCGTATTTCTCATGA
2092_s_at	3419	ATTAGATAGTGCATCTTCTGAGGTC
36114_r_at	3420	GAACAGCTCCGGGCCCCGGTCTGCCT
36114_r_at	3421	CTCCGGGCCCCGGTCTGCCTGGCTGC
36114_r_at	3422	TCCGGGCCCCGGTCTGCCTGGCTGCC
36114_r_at	3423	GGGCCCCGGTCTGCCTGGCTGCCTCC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36114_r_at	3424	CCCGGTCTGCCTGGCTGCCTCCATC
36114_r_at	3425	CGGTCTGCCTGGCTGCCTCCATCAC
36114_r_at	3426	GGTCTGCCTGGCTGCCTCCATCACA
36114_r_at	3427	GTCTGCCTGGCTGCCTCCATCACAG
36114_r_at	3428	GCCTGGCTGCCTCCATCACAGCCCT
36114_r_at	3429	CCTGGCTGCCTCCATCACAGCCCTC
36114_r_at	3430	GTTTCGACCTGATGGCGAAGCTGAAA
36114_r_at	3431	CGACCTGATGGCGAAGCTGAAACAG
36114_r_at	3432	CATCAGCCACGCCCAGAAGTTCCGG
36114_r_at	3433	TCAGCCACGCCCAGAAGTTCCGGAA
36114_r_at	3434	GCCACGCCCAGAAGTTCCGGAAGGG
36114_r_at	3435	GCCCAGAAGTTCCGGAAGGGGGCAG
408_at	3436	GTTTTACAGTGTTTCTGGCTTAGAA
408_at	3437	TTTACAGTGTTTCTGGCTTAGAACA
408_at	3438	GTTTCTGGCTTAGAACAAAGGGGCT
408_at	3439	TTCTGGCTTAGAACAAAGGGGCTTA
408_at	3440	ATTAACCTCTACCTGCACACTGTCCT
408_at	3441	TTTGAAATGTCAACCCCAAGTTAGT
408_at	3442	ATGTTTTCAAATGTTCTCCAGTCAT
408_at	3443	TTTCAAATGTTCTCCAGTCATTATG
408_at	3444	TCAAATGTTCTCCAGTCATTATGTT
408_at	3445	ATATTTCTGAGGAGCCTGCAACATG
408_at	3446	GAGGAGCCTGCAACATGCCAGCCAC
408_at	3447	CTGGCGGATCCAAGCAAATGGCCAA
408_at	3448	CGGATCCAAGCAAATGGCCAATGAG
408_at	3449	TGTGCACATCTGTTTTGTAAGTGT
408_at	3450	TGCACATCTGTTTTGTAAGTGTTA
408_at	3451	CACATCTGTTTTGTAAGTGTTAGA
36058_at	3452	ATCCCATCCTGAGACCTGGTGCAGG
36058_at	3453	CCCATCCTGAGACCTGGTGCAGGGC
36058_at	3454	CATCCTGAGACCTGGTGCAGGGCCA
36058_at	3455	ATCCTGAGACCTGGTGCAGGGCCAG
36058_at	3456	GGAGGCAGCGGCACCAGACTCACCA
36058_at	3457	GAGGCAGCGGCACCAGACTCACCA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36058_at	3458	AGGCAGCGGCACCAGACTCACCAGG
36058_at	3459	TCGCCTGGGGCCTCCTCACTAGGGG
36058_at	3460	GCCATGAGCGCCTTCCTGCAGAACA
36058_at	3461	ATGAGCGCCTTCCTGCAGAACACAC
36058_at	3462	GAGCGCCTTCCTGCAGAACACACAG
36058_at	3463	CAGAACACACAGTGCCTTATGCCAC
36058_at	3464	CTTTACCCTGGACAGCAGGAAACCT
36058_at	3465	TTACCCTGGACAGCAGGAAACCTGT
36058_at	3466	CCCTGGACAGCAGGAAACCTGTATA
36058_at	3467	CTGGACAGCAGGAAACCTGTATATT
34342_s_at	3468	ATTAGATAGTGCATCTTCTGAGGTC
34342_s_at	3469	TTAGATAGTGCATCTTCTGAGGTCA
34342_s_at	3470	TAGATAGTGCATCTTCTGAGGTCAA
34342_s_at	3471	AGATAGTGCATCTTCTGAGGTCAAT
34342_s_at	3472	ATAGTGCATCTTCTGAGGTCAATTA
34342_s_at	3473	AGTGCATCTTCTGAGGTCAATTAAA
34342_s_at	3474	GTGCATCTTCTGAGGTCAATTAAAA
34342_s_at	3475	GCATCTTCTGAGGTCAATTAAAAGG
34342_s_at	3476	CATCTTCTGAGGTCAATTAAAAGGA
34342_s_at	3477	TTAGTTTGTGGCTTCATGGAAACTC
34342_s_at	3478	TAGTTTGTGGCTTCATGGAAACTCC
34342_s_at	3479	GTGGCTTCATGGAAACTCCCTGTAA
34342_s_at	3480	GGCTTCATGGAAACTCCCTGTAAAC
34342_s_at	3481	GCTTCATGGAAACTCCCTGTAAACT
34342_s_at	3482	CTCCCTGTAAACTAAAAGCTTCAGG
34342_s_at	3483	AACTAAAAGCTTCAGGGTTATGTCT
1520_s_at	3484	CTTTCCTGTTGTCTACACCAATGCC
1520_s_at	3485	CCTGCCTTAGGGTAGTGCTAAGAGG
1520_s_at	3486	GAGGATCTCCTGTCCATCAGCCAGG
1520_s_at	3487	TCCATCAGCCAGGACAGTCAGCTCT
1520_s_at	3488	TTTGTGTTGAGCCAGGCCTCTCTCAC
1520_s_at	3489	TTAAAGCCCGCCTGACAGAAACCAC
1520_s_at	3490	GAAACCACGGCCACATTTGGTTCTA
1520_s_at	3491	TAAGAAACCCTCTGTCAATTCGCTCC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1520_s_at	3492	ACATTCTGATGAGCAACCGCTTCCC
1520_s_at	3493	AATTTGGACTGGTGTGCTCTCTTTA
1520_s_at	3494	CAAATATCATACTGTTCAATGGTTC
1520_s_at	3495	ACTTCACCATGCAATTTGTGTCTTC
1520_s_at	3496	ATTTGTGTCTTCCTAAAGAGAGCTG
1520_s_at	3497	TGTACCCAGAGAGTCCTGTGCTGAA
1520_s_at	3498	GACTCAATCCCTAGGGCTGGCAGAA
1520_s_at	3499	GCTATAGCCTGGACTTTCCTGTTGT
38429_at	3500	GGGTCTGCGCTTGGTCTTTCTGTGC
38429_at	3501	TGGTCTTTCTGTGCTTGGATTTGCA
38429_at	3502	TATTGCATTGCTGGTAGAGACCCCC
38429_at	3503	CATTGCTGGTAGAGACCCCCAGGCC
38429_at	3504	CTGCCAAGACTCCTCAGGCAGCGTG
38429_at	3505	AGGCATTGGCTCAGCCCGCTGAGTG
38429_at	3506	TGGGCCCTGCACAGGCACACAGGG
38429_at	3507	CCGGGCACCAACTCCATGTTTGGTG
38429_at	3508	CACCAACTCCATGTTTGGTGTTTGT
38429_at	3509	ACTCCATGTTTGGTGTTTGTCTGTG
38429_at	3510	AATTTACTGTAAGTGTGAGTGTACA
38429_at	3511	ATTTACTGTAAGTGTGAGTGTACAC
38429_at	3512	TAAGTGTGAGTGTGAGTGTGAC
38429_at	3513	GTCAGTGTGAGTGTGAGTGTGAC
38429_at	3514	GTGTACACGTCTGGACCCCGTTTCA
38429_at	3515	GTACACGTCTGGACCCCGTTTCATT
502_s_at	3516	TTCATGTGTGTGAGTTTGCTGGTTG
502_s_at	3517	GTGTGTGAGTTTGCTGGTTGTAAAT
502_s_at	3518	GAGTTTGCTGGTTGTAAATACTTTG
502_s_at	3519	AATACTTTGTCCTAAGAGATTTATC
502_s_at	3520	TACTTTGTCCTAAGAGATTTATCTT
502_s_at	3521	TTGTCCTAAGAGATTTATCTTTATA
502_s_at	3522	TATCTTTATACAGATTTTCTAGAAA
502_s_at	3523	TCTTTATACAGATTTTCTAGAAATG
502_s_at	3524	TTATACAGATTTTCTAGAAATGTTT
502_s_at	3525	TGGGCAAACCTCTCTAAACTGGTACA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
502_s_at	3526	GGCAAACCTCTCTAAACTGGTACAAT
502_s_at	3527	ACTCTCTAAACTGGTACAATTTTAT
502_s_at	3528	TGCCTCAGAGGGTAGCCTTGATTTG
502_s_at	3529	CCTCAGAGGGTAGCCTTGATTTGTT
502_s_at	3530	CAGAGGGTAGCCTTGATTTGTTCTT
502_s_at	3531	GAGGGTAGCCTTGATTTGTTCTTAC
33802_at	3532	TTCTTTCTAGAGAGGGAATTCTCTT
33802_at	3533	ACTGTGTCCCTCTCTCTGGAAAGGA
33802_at	3534	GGAGCCTATGGCATCTTCCCCAACG
33802_at	3535	CCCAACGAAAAGCACATCCAGGCAA
33802_at	3536	CACATCCAGGCAATGGCCTAAACTT
33802_at	3537	GGCAATGGCCTAAACTTCAGAGGGG
33802_at	3538	CAGCATCCTCAGTTCCTGCAGCAGA
33802_at	3539	AGTTCCTGCAGCAGAGCCTGGAAGA
33802_at	3540	TGCAGCAGAGCCTGGAAGACACCCT
33802_at	3541	AGAGCCTGGAAGACACCCTAATGTG
33802_at	3542	TGGAAGACACCCTAATGTGGCAGCT
33802_at	3543	GGCAGCTGTCTCAAACCTCCAAAAG
33802_at	3544	AAGTATCCTTGTTGACACGGCCATG
33802_at	3545	TTTACACAAACCTGAAAAGATGTTG
33802_at	3546	TCAGCCTCAAATGCAGTATTTTTGT
33802_at	3547	GTGTTTAACGGCACTGTGGCCTTGG
38010_at	3548	TGCAACCTTAATTCAGCTGAAGTAC
38010_at	3549	GCAACCTTAATTCAGCTGAAGTACT
38010_at	3550	TGTGGCCTTATATATCACACTATTG
38010_at	3551	GGCCTTATATATCACACTATTGTAG
38010_at	3552	TCAACAGAAACCAAGATAGAGCTAC
38010_at	3553	AGATAGAGCTACAAACTCAGCTGTA
38010_at	3554	AGCTACAAACTCAGCTGTACAGTTC
38010_at	3555	CTCTTCTTGCTTTTGCATTATAAGG
38010_at	3556	CTTCTTGCTTTTGCATTATAAGGAA
38010_at	3557	TTAAGTCTCCGATTATTAGGTGATC
38010_at	3558	TATTAGGTGATCACCCCTGGATGATC
38010_at	3559	TCCTCTTTATCACTCTGCATTGGTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38010_at	3560	ACTCTGCATTGGTGAATTTAATCCT
38010_at	3561	GGTGAATTTAATCCTCTCCTTTGTG
38010_at	3562	GTGAATTTAATCCTCTCCTTTGTGT
38010_at	3563	CAGCTTTATTCTAAGCAAATCTGTG
41046_s_at	3564	TGCCATCTTAGGTTGCCATGAGCCA
41046_s_at	3565	CTTTAGTTCAATGGACAGACCTCCC
41046_s_at	3566	TAGTTCAATGGACAGACCTCCCAAG
41046_s_at	3567	AGGCAAAACTACCTTCTGACTTGG
41046_s_at	3568	ATTGTTCCCCTATCATAAGAGCTAG
41046_s_at	3569	ATCATAAGAGCTAGGCCAAGCCTAT
41046_s_at	3570	CAAGCCTATGGGACCTTGAGTCATG
41046_s_at	3571	CTTGAGTCATGCAGGATGGGATCTG
41046_s_at	3572	TCTTCCCCATCTTGCATTGGAGGTC
41046_s_at	3573	TTGCATTGGAGGTCCCAGAAAACAA
41046_s_at	3574	CAGAAAACAATTAGCTTCTGGCAAA
41046_s_at	3575	TTGCTGTTTCCCAGGCTCCTTTTTG
41046_s_at	3576	TATATATTGTTCTGAGGCGCCTGGC
41046_s_at	3577	AGGCGCCTGGCCTGTCCCTTCAGTG
41046_s_at	3578	GCGCCTGGCCTGTCCCTTCAGTGAG
41046_s_at	3579	AGTGAGAAGCTGTTGTCACGACTAA
39095_at	3580	CCGCAAGGTGCAGCACGAGCTGGAT
39095_at	3581	CGTGACATTGGCACGAAGGGCTTGA
39095_at	3582	GTGACATTGGCACGAAGGGCTTGAA
39095_at	3583	TGACATTGGCACGAAGGGCTTGAAT
39095_at	3584	GACATTGGCACGAAGGGCTTGAATG
39095_at	3585	ACATTGGCACGAAGGGCTTGAATGA
39095_at	3586	TGAGGAGTAGCTTTGCCACATCTTG
39095_at	3587	AGTAGCTTTGCCACATCTTGATCTG
39095_at	3588	TAGCTTTGCCACATCTTGATCTGCT
39095_at	3589	GCTTTGCCACATCTTGATCTGCTCA
39095_at	3590	TTTGCCACATCTTGATCTGCTCAGC
39095_at	3591	TTGCCACATCTTGATCTGCTCAGCC
39095_at	3592	CTTGATCTGCTCAGCCCTGGAGGTG
39095_at	3593	TCTGCTCAGCCCTGGAGGTGCCAGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39095_at	3594	CAGCCCTGGAGGTGCCAGCAAAGCC
39095_at	3595	CCTGGAGGTGCCAGCAAAGCCCCAT
39402_at	3596	ACGGCTATAGCCTGGACTTTCCTGT
39402_at	3597	ACTGCCTGCCTTAGGGTAGTGCTAA
39402_at	3598	AGGACAGTCAGCTCTCTCCTTTCAG
39402_at	3599	GGACAGTCAGCTCTCTCCTTTCAGG
39402_at	3600	GTCAGCTCTCTCCTTTCAGGGCCAA
39402_at	3601	TTTTGTTGAGCCAGGCCTCTCTCAC
39402_at	3602	TTAAAGCCCGCCTGACAGAAACCAC
39402_at	3603	CTGACAGAAACCACGGCCACATTTG
39402_at	3604	CACGGCCACATTTGGTTCTAAGAAA
39402_at	3605	AGTAGCAGTGTCTGTAAAAGAGCCT
39402_at	3606	GTAGCAGTGTCTGTAAAAGAGCCTA
39402_at	3607	ATCAATTCAATTTGGACTGGTGTGC
39402_at	3608	GTGTGCTCTCTTTAAATCAAGTCCT
39402_at	3609	TGAGCAAATATCATACTGTTCAATG
39402_at	3610	AATGTGGACTCAATCCCTAGGGCTG
39402_at	3611	AATCCCTAGGGCTGGCAGAAAGGGA
37184_at	3612	GTGGCTCCTGTTGTCTTGCGCTCTG
37184_at	3613	CGCTCTGGGAAGTCAGATGTCATTT
37184_at	3614	TCAGATGTCATTTCAGGCCTGCAGT
37184_at	3615	ATCCTCCCATCGATGTGCCACGTGG
37184_at	3616	CACGTGGGTGTCACGTGTCCCAGAT
37184_at	3617	CCCAGATGCAGTATTCGGCAGCCAG
37184_at	3618	CCACCTTGGGGCTTCTCATGGGAAA
37184_at	3619	ACCTTGGGGCTTCTCATGGGAAATG
37184_at	3620	GCTTCTCATGGGAAATGTGCCCCCG
37184_at	3621	TCGGCTTTACTCCTGCCCAGTGACT
37184_at	3622	CGGCTTTACTCCTGCCCAGTGACTG
37184_at	3623	TTACTCCTGCCCAGTGACTGTGACC
37184_at	3624	ACTGTGACCACTGTCCGTGTTGCCT
37184_at	3625	TTACCAAAGGTCTTGGTACAACCA
37184_at	3626	TCTTGGTACAACCAGCTGCCCATTT
37184_at	3627	ACCAGCTGCCCATTTTGTGAAATTT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38273_at	3628	CAAGCCCAGGGCATAGATGCTGAGA
38273_at	3629	TCTCCCTCTCAGTGCAGGGACGTCA
38273_at	3630	CTCTCCCTCTCAGTGTGAGGCTTCA
38273_at	3631	TCTCAGTGCGGGAACGTCACCCCTG
38273_at	3632	GGGCACAGATGCTGCGATGGCCTCT
38273_at	3633	TGCGATGGCCTCTTCCTCTTAAGTG
38273_at	3634	ATGGCCTCTTCCTCTTAAGTGTGGG
38273_at	3635	AATTGTATTTCCATATTGAAGCAGC
38273_at	3636	ATTGTATTTCCATATTGAAGCAGCT
38273_at	3637	GTATTTCCATATTGAAGCAGCTTGA
38273_at	3638	CCATATTGAAGCAGCTTGAGTTTCT
38273_at	3639	TATTGAAGCAGCTTGAGTTTCTACT
38273_at	3640	TGAAGCAGCTTGAGTTTCTACTGAA
38273_at	3641	CTGGCATTCTGAGAATTAGACTGAA
38273_at	3642	AAATTGAGGCTCCACGGAGGCCCGT
38273_at	3643	GCATTTTCGCTTTTCAGTAAAAACAG
35894_at	3644	TAGCCACATCTCAGCAAGGAAACTA
35894_at	3645	AGCCACATCTCAGCAAGGAAACTAG
35894_at	3646	GGAAAATCTGTATCCTTGCTGGAAA
35894_at	3647	AAATCTGTATCCTTGCTGGAAACCA
35894_at	3648	TGTATCCTTGCTGGAAACCAGGGCA
35894_at	3649	GTATCCTTGCTGGAAACCAGGGCAG
35894_at	3650	ATCCTTGCTGGAAACCAGGGCAGTG
35894_at	3651	CCTTGCTGGAAACCAGGGCAGTGCA
35894_at	3652	CTTGCTGGAAACCAGGGCAGTGCAC
35894_at	3653	GGAAACCAGGGCAGTGCACATATAA
35894_at	3654	AACCAGGGCAGTGCACATATAAGAG
35894_at	3655	CCAGGGCAGTGCACATATAAGAGTA
35894_at	3656	GGAAGACCATGTAGCAGCTGTGTGA
35894_at	3657	GAAGACCATGTAGCAGCTGTGTGAG
35894_at	3658	AAGACCATGTAGCAGCTGTGTGAGA
35894_at	3659	AGACCATGTAGCAGCTGTGTGAGAG
33429_at	3660	TAAGGCTTTTAGTCCCACCGACATT
33429_at	3661	CCGACATTAGCCAGGCTCGTAGTGA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
33429_at	3662	CAGAGCAGGTTGTGCTGTCCCCTGC
33429_at	3663	CCCTGCCTCTGGAAGCAATGGGGAA
33429_at	3664	CCTCTGGAAGCAATGGGGAATTTGG
33429_at	3665	AATTTGGAATCTTGTGTAAGTGCCC
33429_at	3666	TTTGGAATCTTGTGTAAGTGCCCAA
33429_at	3667	GTGTAAGTGCCCAAATAAGTCTGAG
33429_at	3668	CAAATAAGTCTGAGTGCTTTCCTCT
33429_at	3669	CAATCCCTTAGCACTGATTGATTAG
33429_at	3670	AGCACTGATTGATTAGAGAGGTCCC
33429_at	3671	TCATTGGATGGGTCATAATGTTCCA
33429_at	3672	GGTCATAATGTTCCATGAAACCTCT
33429_at	3673	CAAGTACACAATTGTATGTTCTTTG
33429_at	3674	CTTTTGCAGCTTCCTATAAAGTTTG
33429_at	3675	GCAGCTTCCTATAAAGTTTGTCTTC
558_at	3676	GGTGTCAAGTCCTCTGGTGGCAGTT
558_at	3677	TCTGGTGGCAGTTCCAGCGTGAGGT
558_at	3678	AGAGATGCCCTCTGTTTCATTAGCT
558_at	3679	TGTTTCATTAGCTCTAGTTCTCCCC
558_at	3680	TCACTAACAAATATGCTTGGCAAGA
558_at	3681	ATGCTTGGCAAGACCGAGGTCGATT
558_at	3682	TGGTTAGTTACACTAGCTCATCCTA
558_at	3683	GTTACACTAGCTCATCCTATTCCCC
558_at	3684	GAAGTTTTTCAGATCAGTGGCAATCT
558_at	3685	TCAGTTCCCTTGCTATGACCCTGCT
558_at	3686	CGAGAAACAGTTCAGCAGTGACCAC
558_at	3687	ACATGACATTTCAAGCACCACTTA
558_at	3688	CATTTCAAGCACCACTTAAGCCAG
558_at	3689	AAGCCAGCCAGAGTAGGACCAGTTA
558_at	3690	TGGACAGCTCCTTGCATCTTAACAC
558_at	3691	GCTCCTTGCATCTTAACACTGTGCT
41575_at	3692	GCCACTTATGGATTTCCACACAGCA
41575_at	3693	TCCCAGCTCCACATTAAGACACAGG
41575_at	3694	CATTAAGACACAGGATCTTAAAAGT
41575_at	3695	TACATATCACCTTTGTTGAAGCTAG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
41575_at	3696	CCTTTGTTGAAGCTAGCAAAATGGC
41575_at	3697	ACGATAGTCATACCACAAAAGATAG
41575_at	3698	TACCACAAAAGATAGCATAGCTAGG
41575_at	3699	GGGCCTACCTGGTTCGTATCAACACA
41575_at	3700	AGCTTGTTACTGGAATCTTATGTGC
41575_at	3701	TACTGGAATCTTATGTGCATTACAG
41575_at	3702	GGATCAATCCGGTTGCATCCTTCAA
41575_at	3703	GATCAATCCGGTTGCATCCTTCAAT
41575_at	3704	CTTTTGGTTTTTCATTACAGTAGGCT
41575_at	3705	TTTCATTACAGTAGGCTATGTTAGC
41575_at	3706	CAGTAGGCTATGTTAGCCTTTATTT
41575_at	3707	TTATTTTGGTGGTTCTCAAATACCT
39780_at	3708	ATATAGACCTATGATGTACAGGTAC
39780_at	3709	ACCTATGATGTACAGGTACGACATG
39780_at	3710	CAGGTACGACATGTATAGGTTACCT
39780_at	3711	TTTTTGATTAAGCAATGCAGCCTAG
39780_at	3712	TGATTAAGCAATGCAGCCTAGAAGC
39780_at	3713	ATTAAGCAATGCAGCCTAGAAGCAA
39780_at	3714	CAATGCAGCCTAGAAGCAATGGTTC
39780_at	3715	CTGTTCAATCATTTCAGATGTTAGTG
39780_at	3716	AGACTGCATGTTGAAACCTTTCCTT
39780_at	3717	ACTTTGGTGGCCTGCTTCCCTCATG
39780_at	3718	CTTTGGTGGCCTGCTTCCCTCATGC
39780_at	3719	TTTGGTGGCCTGCTTCCCTCATGCC
39780_at	3720	CCTCATGCCCTGGAATACAACCTCAG
39780_at	3721	GAATACAACCTCAGAGCTCCAGGCAG
39780_at	3722	CAGGCAGCGGAACCATCTATTGTTT
39780_at	3723	TGCATGTGCAGGACTATTCGAGTAT
1257_s_at	3724	TTGGCCCTCAACTGGGGCAAGTGAA
1257_s_at	3725	CTCAACTGGGGCAAGTGAAGCCAGA
1257_s_at	3726	CAACTGGGGCAAGTGAAGCCAGAGG
1257_s_at	3727	CTGCTCCTTCCGGACAATGAAGAAG
1257_s_at	3728	CTCCTTCCGGACAATGAAGAAGCCT
1257_s_at	3729	CTTCCGGACAATGAAGAAGCCTTTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1257_s_at	3730	ATGAAGAAGCCTTTGCACCCTGGGA
1257_s_at	3731	AGAAGCCTTTGCACCCTGGGAGGAA
1257_s_at	3732	TTTGCACCCTGGGAGGAAGGACCAC
1257_s_at	3733	GGTTTGGGAAGCTTCTGGAAGTCGTG
1257_s_at	3734	TTGGAAGCTTCTGGAAGTCGTGCTG
1257_s_at	3735	GGAAGCTTCTGGAAGTCGTGCTGGT
1257_s_at	3736	AGCTTCTGGAAGTCGTGCTGGTCTC
1257_s_at	3737	TTCTGGAAGTCGTGCTGGTCTCCCA
1257_s_at	3738	CTGGAAGTCGTGCTGGTCTCCCAGG
1257_s_at	3739	GAAGTCGTGCTGGTCTCCCAGGTGA
32904_at	3740	GGTTTACACGCTAATCCCGATTAC
32904_at	3741	ATTCTCAAGCCCTGCAGTCACAGCT
32904_at	3742	TTCTCAAGCCCTGCAGTCACAGCTA
32904_at	3743	GATCACAGCTTCAGCCAGGAGCTGG
32904_at	3744	AGCTTCAGCCAGGAGCTGGGCAGAA
32904_at	3745	AGGCCAAGAGGCTGTTCCCACCAGG
32904_at	3746	GCCAAGAGGCTGTTCCCACCAGGCT
32904_at	3747	ACCAGGCTGCTCAGGGCTGGTCTTT
32904_at	3748	GCTGCTCAGGGCTGGTCTTTTAGGA
32904_at	3749	TCAGGGCTGGTCTTTTAGGACCCTT
32904_at	3750	TCCCTTGAGCCCTCTATGGTGTGGC
32904_at	3751	CTATGGTGTGGCAAAGCCTTCATTG
32904_at	3752	TGTGGCAAAGCCTTCATTGCCTTAA
32904_at	3753	TGCCTTAACTGGAGCCCCATCAGCT
32904_at	3754	ATCAGCTCCAGCTGCTCTGTCTTCT
32904_at	3755	CTGTCCTGACCTGTCTCACCATGTA
31499_s_at	3756	GCTACTTCATTGACGCTGCCACAGT
31499_s_at	3757	TGGAGAGTACAGGTGCCAGACAAAC
31499_s_at	3758	TACAGGTGCCAGACAAACCTCTCCA
31499_s_at	3759	TCAGTGACCCGGTGCAGCTAGAAGT
31499_s_at	3760	GAGGAAGACCCTATTACCTGAGGT
31499_s_at	3761	GGTCACATATTTACAGAATGGCAAA
31499_s_at	3762	AAATGTGTCTTCAGAGACTGTGAAC
31499_s_at	3763	GGCAGTGTCAACCATCTCATCATTC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31499_s_at	3764	CAAGTCTCTTTCTGCTTGGTGATGG
31499_s_at	3765	TGGTACTCCTTTTTGCAGTGGACAC
31499_s_at	3766	ACACAGGACTATATTTCTCTGTGAA
31499_s_at	3767	GACAAACATTTGAAGCTCAACAAGA
31499_s_at	3768	CTCAACAAGAGACTGGAAGGACCAT
31499_s_at	3769	GAGAAAGGACCCTCAAGACAAATGA
31499_s_at	3770	GAAAGGACCCTCAAGACAAATGACC
31499_s_at	3771	GCAGCAGCATCTCTGAACATTTCTC
1069_at	3772	GGTTGAATGTTTGTCTTAGGATAG
1069_at	3773	ATGTTTGTCTTAGGATAGGCCTAT
1069_at	3774	AGGATAGGCCTATGTGCTAGCCCAC
1069_at	3775	TGTGCTAGCCCACAAAGAATATTGT
1069_at	3776	AGCCCACAAAGAATATTGTCTCATT
1069_at	3777	ATATTGTCTCATTAGCCTGAATGTG
1069_at	3778	TCTCATTAGCCTGAATGTGCCATAA
1069_at	3779	GTTTTGAGGGATCTGTGGATGCTTC
1069_at	3780	ATGCTTCGTTAATTTGTTTCAGCCAC
1069_at	3781	CGTTAATTTGTTTCAGCCACAATTA
1069_at	3782	TTTGTTTCAGCCACAATTTATTGAGA
1069_at	3783	CAGCCACAATTTATTGAGAAAATAT
1069_at	3784	TTCTGTGTCAAGCACTGTGGGTTTT
1069_at	3785	TTTTAAATCAAACGCTGATTACAGA
1069_at	3786	TATCATTAAAGATAACTCAGGAGAA
1069_at	3787	TAAGTCAGGAGAATCTTCTTTACAA
39413_at	3788	AATTATACTACTTCTAAGGTAGCTG
39413_at	3789	TTATACTACTTCTAAGGTAGCTGCA
39413_at	3790	ATACTACTTCTAAGGTAGCTGCAGA
39413_at	3791	ACTACTTCTAAGGTAGCTGCAGATA
39413_at	3792	TACTTCTAAGGTAGCTGCAGATAAG
39413_at	3793	CTTCTAAGGTAGCTGCAGATAAGTG
39413_at	3794	TCTAAGGTAGCTGCAGATAAGTGGC
39413_at	3795	CTAAGGTAGCTGCAGATAAGTGGCC
39413_at	3796	AAGGTAGCTGCAGATAAGTGGCCTT
39413_at	3797	AGGTAGCTGCAGATAAGTGGCCTTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39413_at	3798	TAGCTGCAGATAAGTGGCCTTGACA
39413_at	3799	AGCTGCAGATAAGTGGCCTTGACAC
39413_at	3800	GCTGCAGATAAGTGGCCTTGACACA
39413_at	3801	AGATAAGTGGCCTTGACACATTACA
39413_at	3802	ATAAGTGGCCTTGACACATTACAAG
39413_at	3803	AAGTGGCCTTGACACATTACAAGCC
34281_at	3804	TTGGACAGACACAGAGGGACCCTTG
34281_at	3805	CCTTGGCTCCTGTGTCTGGTCCACA
34281_at	3806	CTTGGCTCCTGTGTCTGGTCCACAC
34281_at	3807	TGGCTCCTGTGTCTGGTCCACACAC
34281_at	3808	TGTCTGGTCCACACACCACAGAAGC
34281_at	3809	GTCCACACACCACAGAAGCTTGTAT
34281_at	3810	ACACCACAGAAGCTTGTATTATCAG
34281_at	3811	CACCACAGAAGCTTGTATTATCAGT
34281_at	3812	ACCACAGAAGCTTGTATTATCAGTG
34281_at	3813	GTACTACATTTGCATGCCTTTTGGG
34281_at	3814	ATTTGCATGCCTTTTGGGTTTGCCT
34281_at	3815	TTGCATGCCTTTTGGGTTTGCCTTA
34281_at	3816	GGGTTTGCCTTAATTCTTACCTCAT
34281_at	3817	CCTGCTAAATGACTTATTGATTAAG
34281_at	3818	TTAAAATTGCAGCAGTTGCTAGCAA
34281_at	3819	AATTGCAGCAGTTGCTAGCAACAAC
33914_r_at	3820	GAGATTCATAAATCTTCTATATTGA
33914_r_at	3821	TAAATCTTCTATATTGAGAATTGGC
33914_r_at	3822	AATCTTCTATATTGAGAATTGGCTA
33914_r_at	3823	TCTTCTATATTGAGAATTGGCTATG
33914_r_at	3824	TAAGTTTGATTTCATGCTGTCTGTTA
33914_r_at	3825	AGTTTGATTTCATGCTGTCTGTAAAT
33914_r_at	3826	GTTTGATTTCATGCTGTCTGTAAAT
33914_r_at	3827	ATTCATGCTGTCTGTAAATCAAAA
33914_r_at	3828	TCATGCTGTCTGTAAATCAAACT
33914_r_at	3829	CTCATGAGTAGCATCCACATTTTAA
33914_r_at	3830	TCATGAGTAGCATCCACATTTTAA
33914_r_at	3831	CATGAGTAGCATCCACATTTTAAA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
33914_r_at	3832	GTAGCATCCACATTTTTAAAATTTC
33914_r_at	3833	AGCATCCACATTTTTAAAATTTC
33914_r_at	3834	CATCCACATTTTTAAAATTTC
33914_r_at	3835	TCCACATTTTTAAAATTTC
35762_at	3836	TGAGACTAGCAATTAGTTGGCTGCT
35762_at	3837	CTAGCAATTAGTTGGCTGCTCCCTA
35762_at	3838	AATATGACAGGCTTAAGTACTGCTG
35762_at	3839	ATGACAGGCTTAAGTACTGCTGTCC
35762_at	3840	GGCTTAAGTACTGCTGTCCCTTTG
35762_at	3841	TGCTGTCCCTTTTGCATCTTCCTAAG
35762_at	3842	GCTGTCCCTTTTGCATCTTCCTAAGC
35762_at	3843	GCATCTTCCTAAGCATCTTGGTTAA
35762_at	3844	CCTAAGCATCTTGGTTAAATTTCTG
35762_at	3845	CTAAGCATCTTGGTTAAATTTCTGA
35762_at	3846	TCTATTAGGTCCATTGGCAAAGTAT
35762_at	3847	TCCATTGGCAAAGTATATTGGTCCA
35762_at	3848	TTAAGATTCCTTTATTGTGGTACCA
35762_at	3849	AGATTCCTTTATTGTGGTACCATGT
35762_at	3850	GATTCCTTTATTGTGGTACCATGTC
35762_at	3851	CTCCCGGTACACACACAGGGTACGT
36372_at	3852	TCAAGACCAAGTTCCTCTCTGAGAT
36372_at	3853	CCTCTCTGAGATCGAAAGTGACAGC
36372_at	3854	AGGTCCGAGCCATCCTAGAGGATCT
36372_at	3855	GCTGTGTCCCAGAGGGCTGCCCAGC
36372_at	3856	CCCTCGCTGTGTGGTCACGTTCCCTG
36372_at	3857	CTGTGTGGTCACGTTCCCTGCAGTCA
36372_at	3858	AGGTGCGGCCCTGGTCACCGCTGTT
36372_at	3859	AGTTGACTCGTGTCTGAGGAAACCT
36372_at	3860	TGACTCGTGTCTGAGGAAACCTCCA
36372_at	3861	TCGTGTCTGAGGAAACCTCCAGGCT
36372_at	3862	ACCTCCAGGCTGAGGAGGTCTCCGC
36372_at	3863	CTCCAGGCTGAGGAGGTCTCCGCCG
36372_at	3864	GGCCATTTGGCCTTGCTCCCTGGCT
36372_at	3865	GCCATTTGGCCTTGCTCCCTGGCTT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36372_at	3866	TGGCTTTCCCTGAGAGAAGTAGCAC
36372_at	3867	AGAAGTAGCACTCAGGTTAGCAATA
32451_at	3868	TCCAAAGTTGTTTCCAGAAATTGGT
32451_at	3869	CCACCTACTCCATTGCTTTATGAGG
32451_at	3870	CTCCATTGCTTTATGAGGTTTAAGG
32451_at	3871	AATCCAACCTTCTGACCGCCCAGTAG
32451_at	3872	TTCTGACCGCCCAGTAGGAAGAAAA
32451_at	3873	TGAGACATTTTTTCCATTACAGAGA
32451_at	3874	TCCATTACAGAGAAATGCTTCTTGA
32451_at	3875	TTACAGAGAAATGCTTCTTGACTTT
32451_at	3876	AGAGAAATGCTTCTTGACTTTAACA
32451_at	3877	GAGAAATGCTTCTTGACTTTAACAT
32451_at	3878	AGTGAACCTGCTGGAACCTCACACATG
32451_at	3879	GGAACCTCACACATGCCCTGATATGT
32451_at	3880	TCACACATGCCCTGATATGTAAATG
32451_at	3881	CACACATGCCCTGATATGTAAATGA
32451_at	3882	CATGCCCTGATATGTAAATGATGAT
32451_at	3883	TATGTTGGCGAGTCTGAGAGCAAGC
40385_at	3884	AGGCTGTGACATCAATGCTATCATC
40385_at	3885	AAAGTTGTCTGTGTGCGCAAATCCA
40385_at	3886	GTGTGCGCAAATCCAAAACAGACTT
40385_at	3887	GCGTCTCCTCAGTAAAAAAGTCAAG
40385_at	3888	GGAATTGGACATAGCCCAAGAACAG
40385_at	3889	TGGACATAGCCCAAGAACAGAAAGA
40385_at	3890	CTTGACATCATGGAGGGTTTAGTG
40385_at	3891	TCATAGTTTGCTTTGTTTAAGCATC
40385_at	3892	GCTTTGTTTAAGCATCACATTAAAG
40385_at	3893	TCCATAAGCTATTTTGGTTTAGTGC
40385_at	3894	CCATAAGCTATTTTGGTTTAGTGCA
40385_at	3895	AGATTATATGGACTTTCTTGCAAGC
40385_at	3896	ATTATATGGACTTTCTTGCAAGCAA
40385_at	3897	TGGACTTTCTTGCAAGCAACAAGCT
40385_at	3898	GGACTTTCTTGCAAGCAACAAGCTA
40385_at	3899	TTGTCTCCTAAATTGTTGTAATTGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35036_at	3900	TTAATTCATCCAAATGTACTGAGGT
35036_at	3901	TTACCACACACTTGACTACGGATGT
35036_at	3902	TGACTACGGATGTGATCAACACTAA
35036_at	3903	TTGAGCCAGGGCAGGCCTCAGACAC
35036_at	3904	GCCCGGAATGCCAGTGCTCCGAGCT
35036_at	3905	CGGAATGCCAGTGCTCCGAGCTCAG
35036_at	3906	GCTCCGAGCTCAGACAGAGGAAGCC
35036_at	3907	TCAGACAGAGGAAGCCCTGCAGAAA
35036_at	3908	TTTAGCACAGTTCATAGTCCACAG
35036_at	3909	TTAGCACAGTTCATAGTCCACAGTT
35036_at	3910	CAGTTCATAGTCCACAGTTGATGCA
35036_at	3911	CACAGTTGATGCAGCATCCTGAGAT
35036_at	3912	TTGATGCAGCATCCTGAGATTTTAA
35036_at	3913	TGATGCAGCATCCTGAGATTTTAAA
35036_at	3914	GTGGCGCACACACCAAGTAGGGAGC
35036_at	3915	CGCACACACCAAGTAGGGAGCTAGT
34014_f_at	3916	TTAAAAATGCATGCAAACCTGAAAGC
34014_f_at	3917	GAGTTTGGTTTTTGCAACCGGAGGCA
34014_f_at	3918	AGTTTGGTTTTTGCAACCGGAGGCAG
34014_f_at	3919	GTTTGGTTTTTGCAACCGGAGGCAGA
34014_f_at	3920	TTTGGTTTTTGCAACCGGAGGCAGAG
34014_f_at	3921	TTTTGCAACCGGAGGCAGAGAGAAA
34014_f_at	3922	GCAACCGGAGGCAGAGAGAAAAACG
34014_f_at	3923	CAACCGGAGGCAGAGAGAAAAACGG
34014_f_at	3924	TTCTATTTCTAAGGAACATCTTGAG
34014_f_at	3925	TCTATTTCTAAGGAACATCTTGAGT
34014_f_at	3926	CTATTTCTAAGGAACATCTTGAGTG
34014_f_at	3927	TATTTCTAAGGAACATCTTGAGTGC
34014_f_at	3928	TTTCTAAGGAACATCTTGAGTGCAG
34014_f_at	3929	TTCTAAGGAACATCTTGAGTGCAGA
34014_f_at	3930	TCTAAGGAACATCTTGAGTGCAGAT
34014_f_at	3931	CTAAGGAACATCTTGAGTGCAGATA
37120_at	3932	TCCCTAGTTCGGAAATTCAAGCTAA
37120_at	3933	TTTAAACTGTCACTGCATATGCAAG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37120_at	3934	CGCTCTAATTTTTGGATCATTAAAG
37120_at	3935	AGGTAACAAAACAACCACCTGATAG
37120_at	3936	ACCACCTGATAGTAAGTTTTCTGAT
37120_at	3937	AGAGGTAATCAATTCTTCCGAAGTG
37120_at	3938	CAATGTATTTCTTCATGAGTAAAG
37120_at	3939	AGTATAGATTCCAGTAGCCTAGTTT
37120_at	3940	CAGCACGATAACACCATGACGCCTA
37120_at	3941	GATAACACCATGACGCCTACTGCTG
37120_at	3942	ACCTTGGGATTCTGTGTGCTGCCAT
37120_at	3943	CTGTCAGGCAGCAGCGAAAGCTTGT
37120_at	3944	AGCGAAAGCTTGTTAGGATGTCCTG
37120_at	3945	TTAGGATGTCCTGTGCTGCTTGTGA
37120_at	3946	ATGAGAGCCTCCACACTGTACTGTT
37120_at	3947	GCCTCCACACTGTACTGTTCAAGTC
34013_f_at	3948	GCAACCGGAGGCAGAGAGAAAAACG
34013_f_at	3949	CAACCGGAGGCAGAGAGAAAAACGG
34013_f_at	3950	TTCTATTTCTAAGGAACATCTTGAG
34013_f_at	3951	TCTATTTCTAAGGAACATCTTGAGT
34013_f_at	3952	CTATTTCTAAGGAACATCTTGAGTG
34013_f_at	3953	TATTTCTAAGGAACATCTTGAGTGC
34013_f_at	3954	TTTCTAAGGAACATCTTGAGTGCAG
34013_f_at	3955	TTCTAAGGAACATCTTGAGTGCAGA
34013_f_at	3956	TCTAAGGAACATCTTGAGTGCAGAT
34013_f_at	3957	CTAAGGAACATCTTGAGTGCAGATA
34013_f_at	3958	TCACACACACGCAGACATATGAGTA
34013_f_at	3959	GAGTTTGGTTTTGCAACCGGAGGCA
34013_f_at	3960	AGTTTGGTTTTGCAACCGGAGGCAG
34013_f_at	3961	GTTTGGTTTTGCAACCGGAGGCAGA
34013_f_at	3962	TTTGGTTTTGCAACCGGAGGCAGAG
34013_f_at	3963	TTTTGCAACCGGAGGCAGAGAGAAA
32054_at	3964	AAAGTTCAGGTAGTTCATCTAGTTC
32054_at	3965	AGTTCAGGTAGTTCATCTAGTTCTT
32054_at	3966	GTTTCAGGTAGTTCATCTAGTTCTTC
32054_at	3967	TTCAGGTAGTTCATCTAGTTCTTCC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
32054_at	3968	TCAGGTAGTTCATCTAGTTCTTCCT
32054_at	3969	CAGGTAGTTCATCTAGTTCTTCCTC
32054_at	3970	AGGTAGTTCATCTAGTTCTTCCTCC
32054_at	3971	GGTAGTTCATCTAGTTCTTCCTCCT
32054_at	3972	TAGTTCTTCCTCCTCTGTTAAGCAG
32054_at	3973	GTTCTTCCTCCTCTGTTAAGCAGTA
32054_at	3974	CCCCTGTCACATAACCAGGTGGGCTA
32054_at	3975	CCCTGTCACATAACCAGGTGGGCTAC
32054_at	3976	CCTGTCACATAACCAGGTGGGCTACG
32054_at	3977	CTGTCACATAACCAGGTGGGCTACGG
32054_at	3978	TGTCACATAACCAGGTGGGCTACGGA
32054_at	3979	GTCACATAACCAGGTGGGCTACGGAC
33742_f_at	3980	TTCATATGGCAGCAAGAATTATTGC
33742_f_at	3981	TCATATGGCAGCAAGAATTATTGCC
33742_f_at	3982	AGAATTATTGCCAAGTTAGCAGCTT
33742_f_at	3983	GAATTATTGCCAAGTTAGCAGCTTG
33742_f_at	3984	AATTATTGCCAAGTTAGCAGCTTGG
33742_f_at	3985	ATTATTGCCAAGTTAGCAGCTTGGG
33742_f_at	3986	TTATTGCCAAGTTAGCAGCTTGGGG
33742_f_at	3987	TATTGCCAAGTTAGCAGCTTGGGGA
33742_f_at	3988	ATTGCCAAGTTAGCAGCTTGGGGAA
33742_f_at	3989	TTGCCAAGTTAGCAGCTTGGGGAAA
33742_f_at	3990	TGCCAAGTTAGCAGCTTGGGGAAAA
33742_f_at	3991	GCCAAGTTAGCAGCTTGGGGAAAAG
33742_f_at	3992	CCAAGTTAGCAGCTTGGGGAAAAGA
33742_f_at	3993	ACTCAGCTGAGTTCACAGAGTTCGC
31719_at	3994	CTAAACTGGAGTGATGTTAGCAGAC
31719_at	3995	AGACCCAGCTTAGAGTTCTTCTTTC
31719_at	3996	AGCTTCTCCAAGCATCACCTGGGA
31719_at	3997	GCTTCTCCAAGCATCACCTGGGAG
31719_at	3998	TTTCTCATAAATGAGGGCTGCACA
31719_at	3999	CTGTTCTGCTTCGAAGTATTCAATA
31719_at	4000	GAAGTATTCAATACCGCTCAGTATT
31719_at	4001	GAAAGCATATGCAGCCAACCAAGAT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31719_at	4002	CCAACCAAGATGCAAATGTTTTGAA
31719_at	4003	GGAAAGTCACCCAAACACTTCTGCT
31719_at	4004	ATACTGTAGGAACAAGCATGATCTT
31719_at	4005	CCAAATGATCCTAGTAATTGCCTAG
31719_at	4006	AATGATCCTAGTAATTGCCTAGAAA
31719_at	4007	GATCCTAGTAATTGCCTAGAAATAT
31719_at	4008	TTTTTATACTGTATGTGCCAAAGCT
31719_at	4009	TTTATACTGTATGTGCCAAAGCTTT
35418_at	4010	AGGACCTCTGCTGCTGCCACTGTCA
35418_at	4011	GACCTCTGCTGCTGCCACTGTCATT
35418_at	4012	TCTGCTGCTGCCACTGTCATTGTGG
35418_at	4013	CTGCCACTGTCATTGTGGTTAATGA
35418_at	4014	GCCACTGTCATTGTGGTTAATGATG
35418_at	4015	CCACTGTCATTGTGGTTAATGATGG
35418_at	4016	CACTGTCATTGTGGTTAATGATGGC
35418_at	4017	TTCTTATTCCCGTATCTTTGAGAGA
35418_at	4018	ATTCCTCGTATCTTTGAGAGAGGAAG
35418_at	4019	CCCGTATCTTTGAGAGAGGAAGAGA
35418_at	4020	CCAGGGTGCCTAGACAAGAGGTAGC
35418_at	4021	CAGGGTGCCTAGACAAGAGGTAGCA
35418_at	4022	GGTGCCTAGACAAGAGGTAGCAGCC
35418_at	4023	TGCCTAGACAAGAGGTAGCAGCCTG
35418_at	4024	AGACAAGAGGTAGCAGCCTGTGGAT
35418_at	4025	ACAAGAGGTAGCAGCCTGTGGATGT
1615_at	4026	CCAGTGCCATCAATGGCAACCCATC
1615_at	4027	CCATCAATGGCAACCCATCCTGGCA
1615_at	4028	ACCCATCCTGGCACCTGGCAGACAG
1615_at	4029	CGGTGAATGGAGCCACTGCGCACAG
1615_at	4030	CGCACAGCAGCAGTTTGGATGCCCCG
1615_at	4031	CATTCAGTGACCTGACATCCCAGCT
1615_at	4032	TCACCCCAGGGACAGCATATCAGAG
1615_at	4033	GTCGGATCGCAGCTTGGATGGCCAC
1615_at	4034	TCGCAGCTTGGATGGCCACTTACCT
1615_at	4035	CTTGGATGGCCACTTACCTGAATGA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1615_at	4036	TGGCCACTTACCTGAATGACCACCT
1615_at	4037	TGAATGACCACCTAGAGCCTTGGAT
1615_at	4038	GGAACAATGCAGCAGCCGAGAGCCG
1615_at	4039	ATGCAGCAGCCGAGAGCCGAAAGGG
1615_at	4040	TCCTGACGGGCATGACTGTGGCCGG
1615_at	4041	TGACTGTGGCCGGCGTGGTTCTGCT
1407_g_at	4042	GGGGTAATCACCTTAAAATGTCATC
1407_g_at	4043	ATCACCTTAAAATGTCATCAAAAAT
1407_g_at	4044	CATCAAAAATAGATCTACTAGAAGG
1407_g_at	4045	AGATCTACTAGAAGGCAGCATCACA
1407_g_at	4046	CTACTAGAAGGCAGCATCACATTCC
1407_g_at	4047	TAGAAGGCAGCATCACATTCCCATC
1407_g_at	4048	GGCAGCATCACATTCCCATCTTACT
1407_g_at	4049	CACATTCCCATCTTACTTATGGACT
1407_g_at	4050	TCCCATCTTACTTATGGACTCCTAC
1407_g_at	4051	CCTGGTTCATGTCTTATATGCCTGT
1407_g_at	4052	TTCATGTCTTATATGCCTGTAATGG
1407_g_at	4053	TATATGCCTGTAATGGTTATAAAGC
1407_g_at	4054	GTTATAAAGCCTACCTTCAGGAAAG
1407_g_at	4055	AAAGCCTACCTTCAGGAAAGCTATG
1407_g_at	4056	CTACCTTCAGGAAAGCTATGGTTGA
1407_g_at	4057	TTTAAACATGTCCCTCTACAATAA
31666_f_at	4058	CCTAGAGGTTTCTAGGAGAGAGTAC
31666_f_at	4059	TGTCTCAGATCAAAAATCTTGACCCG
31666_f_at	4060	GTCTCAGATCAAAAATCTTGACCCGA
31666_f_at	4061	TCTCAGATCAAAAATCTTGACCCGAG
31666_f_at	4062	CTCAGATCAAAAATCTTGACCCGAGG
31666_f_at	4063	TCAGATCAAAAATCTTGACCCGAGGC
31666_f_at	4064	CAGATCAAAAATCTTGACCCGAGGCC
31666_f_at	4065	AGATCAAAAATCTTGACCCGAGGCCT
31666_f_at	4066	GATCAAAAATCTTGACCCGAGGCCTC
31666_f_at	4067	ATCAAAAATCTTGACCCGAGGCCTCA
31666_f_at	4068	CACCAATACGTACAGGGAAGATATC
31666_f_at	4069	ACCAATACGTACAGGGAAGATATCT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31666_f_at	4070	GGGCATTATATGCTACCGATATTAG
31666_f_at	4071	GGCATTATATGCTACCGATATTAGG
31666_f_at	4072	GCATTATATGCTACCGATATTAGGA
38299_at	4073	CAGTTTGAATATCCTTTGTTTCAGA
38299_at	4074	GAATATCCTTTGTTTCAGAGCCAGA
38299_at	4075	AATATCCTTTGTTTCAGAGCCAGAT
38299_at	4076	TATCCTTTGTTTCAGAGCCAGATCA
38299_at	4077	ATCCTTTGTTTCAGAGCCAGATCAT
38299_at	4078	TCCTTTGTTTCAGAGCCAGATCATT
38299_at	4079	CCTTTGTTTCAGAGCCAGATCATT
38299_at	4080	GAAAGTGTAGGCTTACCTCAAATAA
38299_at	4081	TGGGCACCTCAGATTGTTGTTGTTA
38299_at	4082	GCATTCCTTCTTCTGGTCAGAAACC
38299_at	4083	CTGGTCAGAAACCTGTCCACTGGGC
38299_at	4084	ACTTATGTTGTTCTCTATGGAGAAC
38299_at	4085	CTTATGTTGTTCTCTATGGAGAACT
38299_at	4086	AAGTGGCTATGCAGTTTGAATATCC
38299_at	4087	AGTGGCTATGCAGTTTGAATATCCT
38299_at	4088	TGCAGTTTGAATATCCTTTGTTTCA
40517_at	4089	GCCTTGGTTGCTTAACATTATTTGT
40517_at	4090	CCTTGGTTGCTTAACATTATTTGTA
40517_at	4091	CCATTATTTTCTGCATCTTGCATGG
40517_at	4092	TTATTTTCTGCATCTTGCATGGTGC
40517_at	4093	TATTTTCTGCATCTTGCATGGTGCA
40517_at	4094	TTTCTGCATCTTGCATGGTGCAACA
40517_at	4095	CATCTTGCATGGTGCAACAATAGAAT
40517_at	4096	TTGCATGGTGCAACAATAGAATATCT
40517_at	4097	CTATGAATTCTAAAGTTCGGCAAAC
40517_at	4098	TGAATTCTAAAGTTCGGCAAACCAA
40517_at	4099	ATATAATTCCAAACACTCAGGTGTG
40517_at	4100	TATAATTCCAAACACTCAGGTGTGT
40517_at	4101	TCCAAACACTCAGGTGTGTGAATGC
40517_at	4102	CACTCAGGTGTGTGAATGCATTAA
40517_at	4103	CATGCAATTCCTTCAATTATGATGG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40517_at	4104	ATGCAATTCCTTCAATTATGATGGA
1350_at	4105	AGGAGCGACTGCTAATCAGTATGGG
1350_at	4106	AGCGACTGCTAATCAGTATGGGGTT
1350_at	4107	GACTGCTAATCAGTATGGGGTTTCC
1350_at	4108	TCAGTATGGGGTTTCTCCCGGGAT
1350_at	4109	TTCTCCCGGGATGGTGAAAATGTT
1350_at	4110	CTCCCGGGATGGTGAAAATGTTCCG
1350_at	4111	AAATGTTCCGGACCTAGATACTGAC
1350_at	4112	TGTTCCGGACCTAGATACTGACGAA
1350_at	4113	TCCGGACCTAGATACTGACGAAGGT
1350_at	4114	AGGTAGCACGACACTGTGAGTGCAC
1350_at	4115	TTGGACACTTTGAAATGGTGAATTT
1350_at	4116	ATTTGCTATTTTATCTCACATACAT
1350_at	4117	TTCTGTCCAGGTTGTTTCATATAATA
1350_at	4118	AATATGCTGTGAGCATCTTTCCATG
1350_at	4119	ATGCTGTGAGCATCTTTCCATGACA
1350_at	4120	CTGTGAGCATCTTTCCATGACATTA
207_at	4121	GATGTGAAGCGACGAGCCATGGCCG
207_at	4122	AAGCGACGAGCCATGGCCGACCCTG
207_at	4123	ATGGCCGACCCTGAGGTGCAGCAGA
207_at	4124	GAGGTGCAGCAGATCATGAGTGACC
207_at	4125	AGTGACCCAGCCATGCGCCTTATCC
207_at	4126	ATGCGCCTTATCCTGGAACAGATGC
207_at	4127	CTCAGCGAACAACCTTAAAGAATCCTG
207_at	4128	GATGTGGGTCTGATTGCAATTCGGT
207_at	4129	ATTGCAATTCGGTGATGACTTGTTT
207_at	4130	CCCTCATGTGGAAAGAGGAGCTGGG
207_at	4131	AGAAGGCCTCATCTCTCTATATTTA
207_at	4132	GACACAGAGACTCGTACCTGCGCTG
207_at	4133	GCTGCCCTCGAGTTCCATGTCTCTT
207_at	4134	CCTCAGGTCCCAGCTGTCTCACGTT
207_at	4135	GTCCCAGCTGTCTCACGTTGTTTAT
207_at	4136	TGTTTATTCTGCGTCCCCTTCTCCA
39166_s_at	4137	CCTGGGCCATAGTCATTCTGCCTGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39166_s_at	4138	CTGGGCCATAGTCATTCTGCCTGCC
39166_s_at	4139	GGCCATAGTCATTCTGCCTGCCCTG
39166_s_at	4140	CCATAGTCATTCTGCCTGCCCTGAA
39166_s_at	4141	AGTCATTCTGCCTGCCCTGAAAGTC
39166_s_at	4142	GCCTGCCCTGAAAGTCCCAGATCAA
39166_s_at	4143	CCTGCCCTGAAAGTCCCAGATCAAG
39166_s_at	4144	CTGCCCTGAAAGTCCCAGATCAAGC
39166_s_at	4145	CCTGAAAGTCCCAGATCAAGCCTGC
39166_s_at	4146	CTGAAAGTCCCAGATCAAGCCTGCC
39166_s_at	4147	GAAAGTCCCAGATCAAGCCTGCCTC
39166_s_at	4148	TTATAGCCAGGTACCTTCTCACCTG
39166_s_at	4149	AGCCAGGTACCTTCTCACCTGTGAG
39166_s_at	4150	GCCAGGTACCTTCTCACCTGTGAGA
39166_s_at	4151	CTCCCAACTATAAACTAGGTGCTG
39166_s_at	4152	AACTATAAACTAGGTGCTGCAGCC
31574_i_at	4153	TTCCAGCCCGGGAGCATCACAGAGG
31574_i_at	4154	TCCAGCCCGGGAGCATCACAGAGGT
31574_i_at	4155	CCAGCCCGGGAGCATCACAGAGGTG
31574_i_at	4156	CAGCCCGGGAGCATCACAGAGGTGT
31574_i_at	4157	CCCGGGAGCATCACAGAGGTGTGCA
31574_i_at	4158	CCGGGAGCATCACAGAGGTGTGCAT
31574_i_at	4159	CGGGAGCATCACAGAGGTGTGCATC
31574_i_at	4160	GGGAGCATCACAGAGGTGTGCATCA
31574_i_at	4161	GAGCATCACAGAGGTGTGCATCACC
31574_i_at	4162	AGCATCACAGAGGTGTGCATCACCT
31574_i_at	4163	GCATCACAGAGGTGTGCATCACCTT
31574_i_at	4164	CATCACAGAGGTGTGCATCACCTTT
31574_i_at	4165	ATCACAGAGGTGTGCATCACCTTTG
40159_r_at	4166	GAAGCGCCTCAGCCAGGACGCCTAT
40159_r_at	4167	GCAACAGCGTCCGTTTTCTGCAGCA
40159_r_at	4168	CCGCCAGGCGCGGCCGGGACCGCAG
40159_r_at	4169	GCCGGGACCGCAGAGCCCCGGGAGC
40159_r_at	4170	CAGAGCCCCGGGAGCCCCGCTCGAGG
40159_r_at	4171	TCGAGGAGGAGCGGCAGACGCAGCG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40159_r_at	4172	TAAACCGCAGCCGGCGGTGCCCCCG
40159_r_at	4173	CGCAGCCGGCGGTGCCCCCGCGGCC
40159_r_at	4174	CCCCCGCGGCCGAGCGCCGACCTCA
40159_r_at	4175	CCTGAACCGCTGCAGCGAGAGCACC
40159_r_at	4176	GAACCGCTGCAGCGAGAGCACCAAG
40159_r_at	4177	CCCCAGCTAGCGTCTCGGCCCTTGC
40159_r_at	4178	TAGCGTCTCGGCCCTTGCCGCCCCG
40159_r_at	4179	CGTCTGGACGCCGAGGGCAGCCCCG
40159_r_at	4180	ACGCCGAGGGCAGCCCCGACCCCTG
40159_r_at	4181	CCCGCCACCCTCAATAAATGTTGCT
33244_at	4182	ATTTGTTCTCCTTGACAAAAGTAG
33244_at	4183	GTGTAAACTCACCAGTCTTGCTTTG
33244_at	4184	ACTCACCAGTCTTGCTTTGGAGTGA
33244_at	4185	CACCAGTCTTGCTTTGGAGTGAGCA
33244_at	4186	CAGTCTTGCTTTGGAGTGAGCAGAA
33244_at	4187	GAATGACTATTTTACGTGGAGCATC
33244_at	4188	TGACTATTTTACGTGGAGCATCATT
33244_at	4189	CTATTTTACGTGGAGCATCATTGTG
33244_at	4190	TACGTGGAGCATCATTGTGTGACTG
33244_at	4191	GAGCATCATTGTGTGACTGTTGACC
33244_at	4192	CATCATTGTGTGACTGTTGACCTGG
33244_at	4193	TGTGTGACTGTTGACCTGGACAGTC
33244_at	4194	ACTGTTGACCTGGACAGTCCCAAGG
33244_at	4195	GTTGACCTGGACAGTCCCAAGGGCT
33244_at	4196	AGTCCCAAGGGCTATGCAGATGGAC
33244_at	4197	TCCCAACTGTACAGATTTGTTTGTT
2041_i_at	4198	CAGTGACATAGTGCAGAGGTAGCAG
2041_i_at	4199	TGACATAGTGCAGAGGTAGCAGCAG
2041_i_at	4200	ACATAGTGCAGAGGTAGCAGCAGTC
2041_i_at	4201	CATAGTGCAGAGGTAGCAGCAGTCA
2041_i_at	4202	ATAGTGCAGAGGTAGCAGCAGTCAG
2041_i_at	4203	TAGTGCAGAGGTAGCAGCAGTCAGG
2041_i_at	4204	CAGAGGTAGCAGCAGTCAGGGGTCA
40635_at	4205	TCACAGATGCCCAGCCTCATAGCTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40635_at	4206	GCCCAGCCTCATAGCTGAAGTTGCC
40635_at	4207	CTGTTGCATGTAACCCACTGGCCTC
40635_at	4208	ACTGGCCTCCCTGAGCATGTCCATT
40635_at	4209	TGGCCTCCCTGAGCATGTCCATTGA
40635_at	4210	TCTCTCCTTGCCAAATAGTTTGTGC
40635_at	4211	CCAAATAGTTTGTGCCTTGTCTTGA
40635_at	4212	TGCCAACCTCACACTGCTATGATTG
40635_at	4213	ACACTGCTATGATTGCCAACTCCAG
40635_at	4214	GATTGCCAACTCCAGCGGTCCCATG
40635_at	4215	ATTGCCAACTCCAGCGGTCCCATGT
40635_at	4216	CAGCGGTCCCATGTCAGCCTTCTGA
40635_at	4217	AGCGGTCCCATGTCAGCCTTCTGAT
40635_at	4218	CATGTCAGCCTTCTGATGATCCCAC
40635_at	4219	TGTCAGCCTTCTGATGATCCCCTC
40635_at	4220	GAATATTTTCCTGACCAAGACTGAG
38908_s_at	4221	ATATTTTCCTCTAGGTTTTGCTTGAC
38908_s_at	4222	ATTTCTCTAGGTTTTGCTTGACTC
38908_s_at	4223	TCCTCTAGGTTTTGCTTGACTCAAA
38908_s_at	4224	CTCTAGGTTTTGCTTGACTCAAAGT
38908_s_at	4225	CAAACAGTAGTACCACGTGTAGCAT
38908_s_at	4226	ACAGTAGTACCACGTGTAGCATTTT
38908_s_at	4227	GTAGTACCACGTGTAGCATTTTGAA
38908_s_at	4228	TACCACGTGTAGCATTTTGAAACAT
38908_s_at	4229	ACCACGTGTAGCATTTTGAAACATT
38908_s_at	4230	CCACGTGTAGCATTTTGAAACATTA
38908_s_at	4231	TTTTGTTACAAACCTGTGGGCCTGT
38908_s_at	4232	GTTACAAACCTGTGGGCCTGTTGCA
38908_s_at	4233	AACCTGTGGGCCTGTTGCAATACTT
38908_s_at	4234	TGGGCCTGTTGCAATACTTTAAAAA
38908_s_at	4235	TCCATTTGCTTGTTTTGTATAGACA
38908_s_at	4236	CCATTTGCTTGTTTTGTATAGACAT
32579_at	4237	TCCAGAGCTGAGATGGCATAGGCCT
32579_at	4238	CATAGGCCTTAGCAGTAACGGGTAG
32579_at	4239	AGCAGTAACGGGTAGCAGCAGATGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
32579_at	4240	ATACAGCAGAGAAGCTGTAGGACTG
32579_at	4241	TAGGACTGTTTGTGACTGGCCCTGT
32579_at	4242	TGTGACTGGCCCTGTCCTGGCATCA
32579_at	4243	TGTCCTGGCATCAGTAGCATCTGTA
32579_at	4244	TCCTGGCATCAGTAGCATCTGTAAC
32579_at	4245	TGGCATCAGTAGCATCTGTAACAGC
32579_at	4246	GCATCAGTAGCATCTGTAACAGCAT
32579_at	4247	CATCAGTAGCATCTGTAACAGCATT
32579_at	4248	TCAGTAGCATCTGTAACAGCATTAA
32579_at	4249	GTAGCATCTGTAACAGCATTAACTG
32579_at	4250	AGCATCTGTAACAGCATTAACTGTC
32579_at	4251	GTAACAGCATTAACTGTCTTAAAGA
32579_at	4252	TAACAGCATTAACTGTCTTAAAGAG
33021_at	4253	CCAAAATGCATCCAAAATAAGATGG
33021_at	4254	GAAGTCAGTACAGCAGAATGGTAAC
33021_at	4255	GTCAGTACAGCAGAATGGTAACAAG
33021_at	4256	GTAACAAGTGAGCATCTCCCTAATG
33021_at	4257	TAACAAGTGAGCATCTCCCTAATGG
33021_at	4258	ACAAGTGAGCATCTCCCTAATGGGA
33021_at	4259	CAAGTGAGCATCTCCCTAATGGGAA
33021_at	4260	TGAGCATCTCCCTAATGGGAATGGG
33021_at	4261	AGCATCTCCCTAATGGGAATGGGAC
33021_at	4262	GCATCTCCCTAATGGGAATGGGACA
33021_at	4263	CTCCCTAATGGGAATGGGACATTCC
33021_at	4264	TCCCTAATGGGAATGGGACATTCT
33021_at	4265	GGAATGGGACATTCTGGTAGAGCT
33021_at	4266	AATGGGACATTCTGGTAGAGCTGG
33021_at	4267	GACATTCTGGTAGAGCTGGGAGAA
33021_at	4268	ACATTCTGGTAGAGCTGGGAGAAA
1125_s_at	4269	AGAAGAGACCCAAATCATTCTGAAG
1125_s_at	4270	ACCCAAATCATTCTGAAGGCTCAAC
1125_s_at	4271	GGTTATACCTCTCATTACCCACACA
1125_s_at	4272	TCATTACCCACACACGAAGGAAAGC
1125_s_at	4273	CCCACACACGAAGGAAAGCAGGACC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1125_s_at	4274	CCTTCATCCCAGTGACCTCAGCTAA
1125_s_at	4275	ATCCCAGTGACCTCAGCTAAGACTG
1125_s_at	4276	ACCTCAGCTAAGACTGGGTCCTTTG
1125_s_at	4277	GCTAAGACTGGGTCCTTTGGAGTTA
1125_s_at	4278	CTGGGTCCTTTGGAGTTACTGCAGT
1125_s_at	4279	TCCTTTGGAGTTACTGCAGTTACTG
1125_s_at	4280	GTTACTGTTGGAGATTCCAACCTCTA
1125_s_at	4281	TGGAGATTCCAACCTCTAATGTCAAT
1125_s_at	4282	ACTCTAATGTCAATCGTTCCTTATC
1125_s_at	4283	ATGTCAATCGTTCCTTATCAGGAGA
1125_s_at	4284	ATCGTTCCTTATCAGGAGACCAAGA
1211_s_at	4285	ACATTACAGGCAGGTGTCTCATATG
1211_s_at	4286	ACAGGCAGGTGTCTCATATGTAAAA
1211_s_at	4287	GGCAGGTGTCTCATATGTAAACAT
1211_s_at	4288	AACATTTACCTGAATGTTGTCTGAG
1211_s_at	4289	TTTACCTGAATGTTGTCTGAGGACT
1211_s_at	4290	ACCTGAATGTTGTCTGAGGACTGAA
1211_s_at	4291	TGTTGTCTGAGGACTGAACTGTGGA
1211_s_at	4292	TGTCTGAGGACTGAACTGTGGACTT
1211_s_at	4293	AGGACTGAACTGTGGACTTTACTAT
1211_s_at	4294	TGAACTGTGGACTTTACTATTTCATA
1211_s_at	4295	TGTGGACTTTACTATTTCATAATGAT
1211_s_at	4296	GGACTTTACTATTTCATAATGATAAA
1211_s_at	4297	TATATCTCATGTCATCACATTACAG
1211_s_at	4298	ATCTCATGTCATCACATTACAGGCA
1211_s_at	4299	TCATGTCATCACATTACAGGCAGGT
1211_s_at	4300	GTCATCACATTACAGGCAGGTGTCT
1445_at	4301	AGTGTTACATCACTAAACTCATCG
1445_at	4302	GCGTTTCTTGATGGGACATTTAGCA
1445_at	4303	TTAGCAAATACCTCTGCCGCTGTT
1445_at	4304	CTCTGCCGCTGTTTCCATCTGCGTA
1445_at	4305	CGCTGTTTCCATCTGCGTAGTAACA
1445_at	4306	GGGCAGTCTGCACAAGGCACATCGA
1445_at	4307	TAAACTAGCATCCACCAAATGCAAG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
1445_at	4308	AGCATCCACCAAATGCAAGAAGAAT
1445_at	4309	TAAACATGGATTTTCATCTTTCTGC
1445_at	4310	GCACTGAATTTGTCTCAGGCACCGT
1445_at	4311	TCTCAGGCACCGTGCAAGGCTCTTT
1445_at	4312	CTTGTCCATAGTGTGGATAGGACTA
1445_at	4313	GGCAGAAGTATTCTCCAGCCCTGG
1445_at	4314	TCTCCAGCCCTGGTAGCATTTGCTC
1445_at	4315	GTAGCATTTGCTCAGAGCCTACGCT
1445_at	4316	CAGAGCCTACGCTTGGTCCAGAACA
1891_at	4317	AATATTCATTTTACTCAGAATAGCC
1891_at	4318	CATTTTACTCAGAATAGCCTGTTTT
1891_at	4319	TTGAGCCTTTATTGGTAAATTCTGG
1891_at	4320	GCTGGACTAGTGTCTTAAAAATGGC
1891_at	4321	CTAGTGTCTTAAAAATGGCTAACTG
1891_at	4322	GCCATCTGACAGACGGCCACTAGTG
1891_at	4323	TTTTATACTGTACATGCTATGCTGA
1891_at	4324	ACTGTACATGCTATGCTGAAGACAT
1891_at	4325	AACTGTGTAAACCACATAATTTTGT
1891_at	4326	TACATCCAAGGATGAGGTGTGACCT
1891_at	4327	GTTTTATATCAAATGCCTTCATGAA
1891_at	4328	TATCAAATGCCTTCATGAATCTTTC
1891_at	4329	TCATGAATCTTTCATACATATATAT
1891_at	4330	ACCCAATACTTTTGTCCAATGTGGT
1891_at	4331	TACTTTTGTCCAATGTGGTTGGTCA
1891_at	4332	TGTCCAATGTGGTTGGTCAAATCAA
31492_at	4333	CCTGGAGCGCTATGTAGAGACGCAG
31492_at	4334	TCACCCTGTGCAAGTGCATGATCGA
31492_at	4335	CCCTGTGCAAGTGCATGATCGACCA
31492_at	4336	TGTGCAAGTGCATGATCGACCAGGC
31492_at	4337	AGTGCATGATCGACCAGGCACATCA
31492_at	4338	GCATGATCGACCAGGCACATCAAGA
31492_at	4339	ACCAGGCACATCAAGAAGAACGGCC
31492_at	4340	AGGCACATCAAGAAGAACGGCCAAT
31492_at	4341	CACATCAAGAAGAACGGCCAATCCG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31492_at	4342	CAATCCGACAGATTTTGTACCTCGG
31492_at	4343	TCCGACAGATTTTGTACCTCGGGGA
31492_at	4344	GCAAGCCCTGGATGAAAACATGGAC
31492_at	4345	ACCAGCACATTGACCGCTGGCTGCT
31492_at	4346	ATGCTCGGGGATCTGTCGGACAGCC
31492_at	4347	GGATCTGTCGGACAGCCAGCTAAAG
31492_at	4348	TCATCTGTAGCCAAGAAGAGAGCAT
31536_at	4349	TGAACTGCACGATAAAGGAACTCAG
31536_at	4350	AACTCAGGCGCCTCTTCTTAGTTGA
31536_at	4351	GCCTCTTCTTAGTTGATGATTAGT
31536_at	4352	GTGGGTATTTACCTATGTTGGTGCC
31536_at	4353	CTTCAGTGTTCCCTGTTATTTATGAA
31536_at	4354	CATTATCTAGGACTTGCAAATAAGA
31536_at	4355	TGCTATGGCTAAAATCCAAGCAAAA
31536_at	4356	GAAGAACGAACCTTGACGTTGCAGT
31536_at	4357	CACAGATCGTTGTTAGATCTTTATT
31536_at	4358	ATTTTATAGCCATGCACTGTTGTGAG
31536_at	4359	AAATTACCTGTCTTGACTGCCATGT
31536_at	4360	AAGCTGCTATGTATGGATTAAACC
31536_at	4361	AGCTGCTATGTATGGATTAAACCG
31536_at	4362	TATCTTTTTCCTATCTGAGGCACTG
31536_at	4363	CTATCTGAGGCACTGGTGGAATAAA
31536_at	4364	TTACTTTGTTGCAGATAGTCTTGC
31955_at	4365	GCCCAGGAGCTACACACCTTCGAGG
31955_at	4366	GGAGCTACACACCTTCGAGGTGACC
31955_at	4367	AAACGGTCGCCCAGATCAAGGCTCA
31955_at	4368	GACGTGACACGCAGCCACGGTCTG
31955_at	4369	GCATTGCCCCGGAAGATCAAGTCGT
31955_at	4370	AAGTCGTGCTCCTGGCAGGCGCGCC
31955_at	4371	GCGCCCCTGGAGGATGAGGCCACTC
31955_at	4372	CCCCTGGAGGATGAGGCCACTCTGG
31955_at	4373	GCAGCCACGGTCTGTACTGACGCG
31955_at	4374	GTGGAGGCCCTGACTACCCTGGAAG
31955_at	4375	CAGGCCGCATGCTTGGAGGTAAAGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
31955_at	4376	TGAGAGGTCAGACTCCTAAGGTGGC
31955_at	4377	GTCAGACTCCTAAGGTGGCCAAACA
31955_at	4378	ACTCTTAAGTCTTTTGTAAATTCTGG
31955_at	4379	CTTTCTCGACTCCATCTTCGCGGTA
31955_at	4380	ATCTTCGCGGTAGCTGGGACCGCCG
32405_at	4381	CATGAGCGACTGTGCCTCTCCAGTC
32405_at	4382	ACTGTGCCTCTCCAGTCCCTGTGTT
32405_at	4383	TTTTGGAGGCACTTTCACTGTGTTG
32405_at	4384	TTTGGAGGCACTTTCACTGTGTTGC
32405_at	4385	GGAGGCACTTTCACTGTGTTGCCCA
32405_at	4386	GTTGCCCAGGCCTGTCTGTTGGCCT
32405_at	4387	TAATTTTGGACTTTGCTCACTAAAG
32405_at	4388	TTTTGGACTTTGCTCACTAAAGTTT
32405_at	4389	TTTGGACTTTGCTCACTAAAGTTTG
32405_at	4390	TTGGACTTTGCTCACTAAAGTTTGA
32405_at	4391	GACTTTGCTCACTAAAGTTTGAATG
32405_at	4392	GTATACAGTCTGGATGCAGTGGTGC
32405_at	4393	TACAGTCTGGATGCAGTGGTGCATG
32405_at	4394	ACAGTCTGGATGCAGTGGTGCATGC
32405_at	4395	AGCCAGACATGATGGCATGCACCTA
32405_at	4396	AGACATGATGGCATGCACCTATAAT
32587_at	4397	TACTGTGACATACTCGAGTATAAAG
32587_at	4398	TGACATACTCGAGTATAAAGACATG
32587_at	4399	GACATACTCGAGTATAAAGACATGT
32587_at	4400	GGGGAGTCTCACAGTGCCTTTGGAA
32587_at	4401	CAGTGCCTTTGGAAGGGCCCGAACT
32587_at	4402	ATGTAGGATGGGTTCAACTGCACAA
32587_at	4403	GATGGGTTCAACTGCACAAAAGGAA
32587_at	4404	CAACTGCACAAAAGGAAAAGATTTT
32587_at	4405	TAAAGTGAAGCAACCGCCTTAGTGC
32587_at	4406	CGCCTTAGTGCTGAAATATGTAGTA
32587_at	4407	TTGTACGTAGGTACAGTTGGAGCAC
32587_at	4408	TACAGTTGGAGCACTATATGTACTC
32587_at	4409	TGTACTCTCTGGACTACTTTGGACA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
32587_at	4410	CTCTGGACTACTTTGGACAGAAGTA
32587_at	4411	CTGGACTACTTTGGACAGAAGTAGG
32587_at	4412	ATATTTTGGGGAATCAGCTCACTAC
32635_at	4413	AACTCACAGAGATCTACTCAGACAG
32635_at	4414	TCACAGAGATCTACTCAGACAGGAC
32635_at	4415	AGGACCTTCGCACCTTTGCCAGAGT
32635_at	4416	ACCTTCGCACCTTTGCCAGAGTTTG
32635_at	4417	GCACCTTTGCCAGAGTTTGAGCAGG
32635_at	4418	GGTAACTGAGGACTCTGATGAAGAC
32635_at	4419	GTAAGTGAAGGACTCTGATGAAGACT
32635_at	4420	GAAGACTTTATACAGCCCCGCAGAA
32635_at	4421	AAACGCCTAAAGTCAGATGAGAGAC
32635_at	4422	ACGCCTAAAGTCAGATGAGAGACCA
32635_at	4423	CGCCTAAAGTCAGATGAGAGACCAG
32635_at	4424	AACAGTCAGGGCTCAGCAGCCTTGT
32635_at	4425	CTCATGCACAGGTCGGCAAGGATTG
32635_at	4426	AAATGAAGACTGGTGTGCTGTCTGC
32635_at	4427	TCCAAGGTACCAGTGAAATAATTGA
32635_at	4428	AACAGGGAGCCTGTTATTCTTTTGG
32719_at	4429	TGAAAGACCTTTCAAACCCCTCGAG
32719_at	4430	GGCCAGCTTCTACAGTACGTCCACT
32719_at	4431	CCTTTCTGTCTCTGCCTGAATAGGA
32719_at	4432	GCTCAGTTGGTGCTGCTTTCTTGTT
32719_at	4433	GCTTTCTTGTTGCTGCATCTCCCCT
32719_at	4434	CCTCTGTTTCGCGACTAGTTGGCTCT
32719_at	4435	CTCTGTTTCGCGACTAGTTGGCTCTG
32719_at	4436	GACTAGTTGGCTCTGAGATACTAAT
32719_at	4437	CTAGTTGGCTCTGAGATACTAATAG
32719_at	4438	GATACTAATAGGTGTGTGAGGCTCC
32719_at	4439	TGAGGCTCCGGATGTTTCTGGAATT
32719_at	4440	CTCCGGATGTTTCTGGAATTGATAT
32719_at	4441	ATACAATGACCACATCCTGAAAAGG
32719_at	4442	CACATCCTGAAAAGGGTGTGCTAA
32719_at	4443	GTGTTGCTAAGCTGTAACCGATATG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
32719_at	4444	TTGCTAAGCTGTAACCGATATGCAC
33371_s_at	4445	CGACCTCTCAGATATTAGGGAGGTT
33371_s_at	4446	AAGGAATACGCTGAATCCATAGGTG
33371_s_at	4447	CTGAATCCATAGGTGCCATCGTGGT
33371_s_at	4448	AGGTGCCATCGTGGTTGAGACAAGT
33371_s_at	4449	TATCGAAGAGCTCTTTCAAGGAATC
33371_s_at	4450	CTCTTTCAAGGAATCAGCCGCCAGA
33371_s_at	4451	TGGACCCCCATGAAAATGGAAACAA
33371_s_at	4452	ACCCCCATGAAAATGGAAACAATGG
33371_s_at	4453	CAGCCGCCGGTGCTGTTGACCCAAG
33371_s_at	4454	CCGCCGGTGCTGTTGACCCAAGGGC
33371_s_at	4455	CCACATCCTGTGCACTGCTGAAGGA
33371_s_at	4456	GTGCACTGCTGAAGGACCCTACGCT
33371_s_at	4457	GGCACCTCACTTTGAGAAGAGTGAG
33371_s_at	4458	GAGCACACTGGCTTTGCATCCTGGA
33371_s_at	4459	GCACACTGGCTTTGCATCCTGGAAG
33371_s_at	4460	ATGGCCTTTAGTGTATGAAATGCAC
33828_at	4461	AGATCACAAAGCTCAAGGAATTTAA
33828_at	4462	GATCACAAAGCTCAAGGAATTTAAT
33828_at	4463	ACTGATTAGCCCATTCAGAAAGAAA
33828_at	4464	CTGATTAGCCCATTCAGAAAGAAA
33828_at	4465	AGAACATCCAAACCTCAAGGCTCAG
33828_at	4466	GAACATCCAAACCTCAAGGCTCAGG
33828_at	4467	CCTCAAGGCTCAGGATCCCATAGAC
33828_at	4468	GAGCCCACCTTTTTGATAAACTTAG
33828_at	4469	AGTTTGTGACACATAAGCTTCCCAA
33828_at	4470	GTTTGTGACACATAAGCTTCCCAA
33828_at	4471	ACTACATATTTGTATGCAAGACAAG
33828_at	4472	TATGCAAGACAAGCATCCAGTTTTT
33828_at	4473	AATGCAGTGACAGTGTGGAATGACC
33828_at	4474	GGAATGACCACTCAGCCATTATAAA
33828_at	4475	GTACAAGACACTTGTGAAAATCAGT
33828_at	4476	ACATTATAGTCATTGTCACAAATGG
35125_at	4477	ACAGACCAAGGAGAACTGGAGAAAG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35125_at	4478	CAGTTCGTGGTTGCATTGTGGATGC
35125_at	4479	GAGCGTTCTCAACTTGGTTATTGTA
35125_at	4480	TGGACTGACTGATACTACAGTGCCT
35125_at	4481	CCTGGGCCCCAAAAGAGCTAGCAGA
35125_at	4482	CCCCAAAAGAGCTAGCAGAATCCGC
35125_at	4483	AAGAGCTAGCAGAATCCGCAAACCTT
35125_at	4484	TTCAATCTCTCTAAAGAAGATGATG
35125_at	4485	GAAACCTAGGACCAAAGCACCCAAG
35125_at	4486	CAAACGGCGGCGTATTGCTCTGAAG
35125_at	4487	AACGGCGGCGTATTGCTCTGAAGAA
35125_at	4488	ACGGCGGCGTATTGCTCTGAAGAAG
35125_at	4489	GCGGCGTATTGCTCTGAAGAAGCAG
35125_at	4490	GCGTATTGCTCTGAAGAAGCAGCGT
35125_at	4491	TTGCTCTGAAGAAGCAGCGTACCAA
35125_at	4492	TGCTCTGAAGAAGCAGCGTACCAAG
35175_f_at	4493	ACCCCAAGTCCCTGAAGTCTGGAGA
35175_f_at	4494	CCCCAAGTCCCTGAAGTCTGGAGAC
35175_f_at	4495	CCAAGTCCCTGAAGTCTGGAGACGC
35175_f_at	4496	GAAAGCCCATGTGTGTGGAGAGCTT
35175_f_at	4497	AAAGCCCATGTGTGTGGAGAGCTTC
35175_f_at	4498	AAGCCCATGTGTGTGGAGAGCTTCT
35175_f_at	4499	AGCCCATGTGTGTGGAGAGCTTCTC
35175_f_at	4500	GCCCATGTGTGTGGAGAGCTTCTCC
35175_f_at	4501	CCCATGTGTGTGGAGAGCTTCTCCC
35175_f_at	4502	CCATGTGTGTGGAGAGCTTCTCCCA
35175_f_at	4503	CGGCGCCGGCAAGGTCACCAAGTCG
35175_f_at	4504	GCGCCGGCAAGGTCACCAAGTCGGC
35434_at	4505	CCTGGCGATGGTCTCAGCAGCCCAG
35434_at	4506	CGATGGTCTCAGCAGCCCAGCCGGG
35434_at	4507	CCCAGAGCCTGAGGCTGAGGGCTC
35434_at	4508	AGGATGCGGCTTGATACCTGGACAT
35434_at	4509	GATGCGGCTTGATACCTGGACATTA
35434_at	4510	GCGGCTTGATACCTGGACATTAAAG
35434_at	4511	CGGCTTGATACCTGGACATTAAAGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
35434_at	4512	TTGATACCTGGACATTAAAGTGACG
35434_at	4513	TGATACCTGGACATTAAAGTGACGA
35434_at	4514	CTCAGCCTCCCTGATGAAGAGTTGA
35434_at	4515	AGCCTCCCTGATGAAGAGTTGACAA
35434_at	4516	CCCCTTCCTTTCTTGTGCTTCGTG
35434_at	4517	TCTTGTGCTTCGTGTCCTGTTGACG
35434_at	4518	CTTGTGCTTCGTGTCCTGTTGACGG
35434_at	4519	TGCTTCGTGTCCTGTTGACGGTTAC
35434_at	4520	TTCGTGTCCTGTTGACGGTTACATT
36331_at	4521	CATACAAATAACACGAGAAGATTG
36331_at	4522	AAGTG TAGATTCTCTTACCCAGTCC
36331_at	4523	GTGTAGATTCTCTTACCCAGTCCTC
36331_at	4524	TCAGTTTCTTCTGAAAACCAGATGG
36331_at	4525	CTTCTGAAAACCAGATGGAGAGATT
36331_at	4526	AGGACTGAAAAACCTCAAGGCCATT
36331_at	4527	TGAAAAACCTCAAGGCCATTGATGT
36331_at	4528	AACCTCAAGGCCATTGATGTAAAGC
36331_at	4529	TCAAGGCCATTGATGTAAAGCTACT
36331_at	4530	GTGTGTACAAAGACTGCAGGGTTTC
36331_at	4531	AAGACTGCAGGGTTTCCATTCCAGC
36331_at	4532	GGGTTTCCATTCCAGCTCCAGCTTT
36331_at	4533	AACTCAA AATTTAGCGTATTTCTGG
36331_at	4534	AGAAGAAACCCCAGTGGGTCATGTG
36331_at	4535	GAAGAAACCCCAGTGGGTCATGTGG
36331_at	4536	ACCCCAGTGGGTCATGTGGTTACCA
36463_at	4537	ACAGGGTGCTCAGCTCTTCCACCGT
36463_at	4538	CCGTCA TTTTGAATTGTTACATGG
36463_at	4539	AATGATCAGATTGACCTTGATTGAC
36463_at	4540	TCAGATTGACCTTGATTGACTGTCA
36463_at	4541	TCTACTCCTGCAATGAACCCTGTTG
36463_at	4542	GACACCGGATTTAGCTCTTGTCGGC
36463_at	4543	ATTTAGCTCTTGTCGGCCTTCGTGG
36463_at	4544	TAATATGAGCTACTGCATGTAATTC
36463_at	4545	AATATGAGCTACTGCATGTAATTCT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36463_at	4546	TATGAGCTACTGCATGTAATTCTTA
36463_at	4547	AGAATCTGTACTGCAAGTAAAACCT
36463_at	4548	TTGGGTCTGCATTAAACGCTGTAGT
36463_at	4549	TAAACGCTGTAGTCCATGTTTCATGC
36463_at	4550	CTGTAGTCCATGTTTCATGCCAAAAA
36463_at	4551	TGTAGTCCATGTTTCATGCCAAAAA
36463_at	4552	CACTTTATCCACACAGGAAAGCCAG
36589_at	4553	CCCCAAGTGACCTATACCTGTGTTT
36589_at	4554	AAGTGACCTATACCTGTGTTTCTTG
36589_at	4555	TGCAAATGTAGTATGGCCTGTGTCA
36589_at	4556	TATGGCCTGTGTCACTCAGCAGTGG
36589_at	4557	CTGTGTCACTCAGCAGTGGGACAGC
36589_at	4558	CCAGCGAGGGCGTGTCTAGCTTGAT
36589_at	4559	GCGTGTCTAGCTTGATGTTGGATCT
36589_at	4560	CTAGCTTGATGTTGGATCTCAAGAG
36589_at	4561	TGATGTTGGATCTCAAGAGCCCTGT
36589_at	4562	GCCCTGTCAAGTAGAGTAGAAGTCTC
36589_at	4563	GAGTAGAAGTCTCTTCCAGTTTGCT
36589_at	4564	GGTTCCCCATGCAGAGGAACTTGGT
36589_at	4565	CCAGGATATGACCACCTTACTCAGC
36589_at	4566	AACAGGAACTGGAGGGTCTGTGCCT
36589_at	4567	AGGGTCTGTGCCTTGTTGAGCTGTA
36589_at	4568	GTETGTGCCTTGTTGAGCTGTACCT
36786_at	4569	GGAGTTGCAGATCAGCTTGAAGAAC
36786_at	4570	GAGTTGCAGATCAGCTTGAAGAACT
36786_at	4571	TTGCAGATCAGCTTGAAGAACTATG
36786_at	4572	AGATCAGCTTGAAGAACTATGATCC
36786_at	4573	CTATGATCCCCAGAAGGACAAGCGC
36786_at	4574	TATGATCCCCAGAAGGACAAGCGCT
36786_at	4575	TCCCCAGAAGGACAAGCGCTTCTCG
36786_at	4576	AAGGACAAGCGCTTCTCGGGCACCG
36786_at	4577	GACAAGCGCTTCTCGGGCACCGTCA
36786_at	4578	CGCTTCTCGGGCACCGTCAGGCTTA
36786_at	4579	TCGGGCACCGTCAGGCTTAAGTCCA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
36786_at	4580	CCGCCCTAAGTTCTCTGTGTGTGTC
36786_at	4581	TTCTCTGTGTGTGTCTGGGGGACC
36786_at	4582	TCTCTGTGTGTGTCTGGGGGACCA
36786_at	4583	TGTCCTGGGGGACCAGCAGCACTGT
36786_at	4584	AGCGCCGCAAGTTCCTGGAGACGGT
37337_at	4585	GTATACACCATGAGCAAAGCTCACC
37337_at	4586	TTAAATGGTGGCAGACATGTCCAAG
37337_at	4587	GTGGCAGACATGTCCAAGGAATATT
37337_at	4588	TGCGGGGATTTGATCCCTTTATGAA
37337_at	4589	GATTTGATCCCTTTATGAACCTTGT
37337_at	4590	TGGAGATGGCGACTAGTGGACAACA
37337_at	4591	AGATGGCGACTAGTGGACAACAGAA
37337_at	4592	TGGCGACTAGTGGACAACAGAACAA
37337_at	4593	AATAGTATCATCATGTTAGAAGCCT
37337_at	4594	TCATCATGTTAGAAGCCTTGGAACG
37337_at	4595	CATCATGTTAGAAGCCTTGGAACGA
37337_at	4596	TGGCTGTTTCAGCAGAGAAACCCATG
37337_at	4597	TTCAGCAGAGAAACCCATGTCCTCT
37337_at	4598	GTCCTCTCTCCATAGGGCCTGTTTT
37337_at	4599	CATAGGGCCTGTTTTACTATGATGT
37337_at	4600	TTTCTAACATGAATTTTCCTGGTTG
37668_at	4601	TCTGAAGCTAGACATGTGCTTTGAA
37668_at	4602	ATGATTATCATCCTAATATCATGGG
37668_at	4603	CTCTATCAGGGAAGTTAGCTTTCAG
37668_at	4604	TCCACTGGCGAGTCTGAATGGAAGG
37668_at	4605	CTGGCGAGTCTGAATGGAAGGATAC
37668_at	4606	CACTCAACACAGATTCCTTGGAAGT
37668_at	4607	AATGGATTTCTTGCCGACCGAGGG
37668_at	4608	GGTGGACAACACTTTTGCAGATGAG
37668_at	4609	ACACTTTTGCAGATGAGCTGGTGGA
37668_at	4610	AGCACCAGGAGTACATTACTTTTCT
37668_at	4611	ACTTTTCTTGAAGACCTCAAGAGTT
37668_at	4612	CTCAAGAGTTTTGTCAAGAGCCAGT
37668_at	4613	AGAGCCAGTAGAGCAGACAGATGCT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
37668_at	4614	AGTGAACAAATCCTACTCTGAAGCT
37668_at	4615	GTGAACAAATCCTACTCTGAAGCTA
37668_at	4616	CTACTCTGAAGCTAGACATGTGCTT
37788_at	4617	CATGAATCACATAGAGCAGTGGAGT
37788_at	4618	AAACTTTTCAAAGACTAGTGTCTGA
37788_at	4619	CCATCATGTTTTATAGTCATTGTTG
37788_at	4620	AGTCATTGTTGCTTCCATTGTTAGT
37788_at	4621	TAAATTCATTTCGTATCTTGTTGGCT
37788_at	4622	AAATTCATTTCGTATCTTGTTGGCTG
37788_at	4623	ATTCATTTCGTATCTTGTTGGCTGCC
37788_at	4624	TCATTTCGTATCTTGTTGGCTGCCTA
37788_at	4625	CATTTCGTATCTTGTTGGCTGCCTAT
37788_at	4626	TTCGTATCTTGTTGGCTGCCTATGA
37788_at	4627	GATTCAGTAGTCATTGTATGCATCT
37788_at	4628	ATTCAGTAGTCATTGTATGCATCTT
37788_at	4629	TCAGTAGTCATTGTATGCATCTTTA
37788_at	4630	TAGTCATTGTATGCATCTTTAAGTC
37788_at	4631	GTCATTGTATGCATCTTTAAGTCAA
37788_at	4632	CTGTTTCCTCTTGTAAGTGCTGATTA
38228_g_at	4633	GCCTCCAAAGTATTGTACAAATAAG
38228_g_at	4634	TGTGCAGTATCTGTGAACTGAATTC
38228_g_at	4635	TGCAGTATCTGTGAACTGAATTCAC
38228_g_at	4636	CTGTGAACTGAATTCACCACAGACT
38228_g_at	4637	GAACTGAATTCACCACAGACTTTAG
38228_g_at	4638	TCACCACAGACTTTAGCTTTCTGAG
38228_g_at	4639	ACTTTAGCTTTCTGAGCAAGAGGAT
38228_g_at	4640	CTTTAGCTTTCTGAGCAAGAGGATT
38228_g_at	4641	AGCTTTCTGAGCAAGAGGATTTTGC
38228_g_at	4642	CTTTCTGAGCAAGAGGATTTTGCGT
38228_g_at	4643	TTCTGAGCAAGAGGATTTTGCGTCA
38228_g_at	4644	TTTTGCGTCAGAGAAATGTCTGTCC
38228_g_at	4645	TTGAGATTTTTATGCCTGTGACTTC
38228_g_at	4646	GATTTTTATGCCTGTGACTTCCTTG
38228_g_at	4647	TTTTTATGCCTGTGACTTCCTTGGA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38228_g_at	4648	GCCTGTGACTTCCTTGGAAATCAAA
38269_at	4649	CACCTTCCCTTTCAACGAGGATGAG
38269_at	4650	GAAGATGCGCAAACGCTACAGCGTG
38269_at	4651	CAGACGTGGCTGGACCTCCGAGAGC
38269_at	4652	GAGAGCGATACATCACGCATGAGAG
38269_at	4653	CACGCATGAGAGTGACGACGCGCGC
38269_at	4654	TCTGGGCTGCCCCACGGACAGGGATC
38269_at	4655	AGCGCATCAGTGTTCTCTGAGGTCC
38269_at	4656	GCATCAGTGTTCTCTGAGGTCCTGT
38269_at	4657	GTTCTCTGAGGTCCTGTGCCCTCGT
38269_at	4658	TTCTCTGAGGTCCTGTGCCCTCGTC
38269_at	4659	TCTGAGGTCCTGTGCCCTCGTCCAG
38269_at	4660	CCTCCACAGCGGTTCTTCACAGGAT
38269_at	4661	CTCCACAGCGGTTCTTCACAGGATC
38269_at	4662	CACAGCGGTTCTTCACAGGATCCCA
38269_at	4663	GGTTCTTCACAGGATCCCAGCAATG
38269_at	4664	TCACAGGATCCCAGCAATGAACTGT
38527_at	4665	TCCCAGGTGAGAATTCAGGCAAACG
38527_at	4666	AGAATTCAGGCAAACGTCCACAAAG
38527_at	4667	GAATTCAGGCAAACGTCCACAAAGG
38527_at	4668	CAGGCAAACGTCCACAAAGGTCACA
38527_at	4669	CACAAAGGTCACAGGCAGCGTACAT
38527_at	4670	AAGGTCACAGGCAGCGTACATACGG
38527_at	4671	GTACATACGGTTCTGTTATACCCCA
38527_at	4672	GGAATGACCCTTTTGTGTCTATGAT
38527_at	4673	GAATGACCCTTTTGTGTCTATGATG
38527_at	4674	GACCCTTTTGTGTCTATGATGTTGC
38527_at	4675	TGTGTCTATGATGTTGCTGTTTACA
38527_at	4676	TTGATAGGCCTAGTACAATCTTGGG
38527_at	4677	ATAGGCCTAGTACAATCTTGGGAAC
38527_at	4678	CTAGTACAATCTTGGGAACAGGGTT
38527_at	4679	GCCTATCTTAGGTAGTCATGCTGTG
38527_at	4680	ATCTTAGGTAGTCATGCTGTGCATT
38590_r_at	4681	TTGTGTATGTACTTAGCTGTACTAT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
38590_r_at	4682	ATGTAAGTCTAGCTGTACTATAAGTAG
38590_r_at	4683	ACTTAGCTGTACTATAAGTAGTTGG
38590_r_at	4684	ATAAGTAGTTGGTTTGTATGAGATG
38590_r_at	4685	TAGTTGGTTTGTATGAGATGGTTAA
38590_r_at	4686	AGTTGGTTTGTATGAGATGGTTAAA
38590_r_at	4687	TTTTCCTTTTTTGTCTATGAAGTTG
38590_r_at	4688	CACTTCCCGTCTCAGAATCTAAACG
38590_r_at	4689	ACTTCCCGTCTCAGAATCTAAACGT
38590_r_at	4690	CACCTTCGAGTAGAGAGGCCCGCCC
38590_r_at	4691	CAACCCAAACCATGAGAATTTGCAA
38590_r_at	4692	TGAGAATTTGCAACAGGGGAGGAAA
38590_r_at	4693	CCAAACCAGCCTTCGGAGCGTTCTC
38590_r_at	4694	CAAACCAGCCTTCGGAGCGTTCTCT
38590_r_at	4695	CCAGCCTTCGGAGCGTTCTCTGTCC
38590_r_at	4696	TCTTATTCCGAGCATTCCAGTAACT
39136_at	4697	ACTTCTTCTGCATGATGTGTGGTAG
39136_at	4698	TCTGCATGATGTGTGGTAGACTCCC
39136_at	4699	ACAGCACGTAACCTAGTGAGTGACT
39136_at	4700	CGTAACCTAGTGAGTGACTGTACTC
39136_at	4701	AGTGACTGTACTCCTTTCTAGGAAT
39136_at	4702	TGTACTCCTTTCTAGGAATGCTGAT
39136_at	4703	CCTTTCTAGGAATGCTGATTCAGAG
39136_at	4704	TGCTGATTCAGAGTGCACCTCTTTG
39136_at	4705	AGGATCCCCTTGTCCTGGAGTAGG
39136_at	4706	TTGTCCCTGGAGTAGGGACTAACTA
39136_at	4707	TGATGTACCAATAAGTGGAGATTCC
39136_at	4708	ATAAGTGGAGATTCCTCCTTATGAT
39136_at	4709	AAGTGGAGATTCCTCCTTATGATGT
39136_at	4710	TGGAGATTCCTCCTTATGATGTATG
39136_at	4711	GGAGATTCCTCCTTATGATGTATGC
39136_at	4712	GATTCCTCCTTATGATGTATGCTAG
39155_at	4713	TTGACATCTATTCCACCCGAGAGCC
39155_at	4714	CAGCGCATCTCCTTCTGCCTAGATA
39155_at	4715	CGAGAACAGCAGGACTTGGAGTTTG

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
39155_at	4716	CAGGACTTGGAGTTTGCCAAGGAGA
39155_at	4717	GATGATGACAGCTTCCCTTGAGCTG
39155_at	4718	ATGATGACAGCTTCCCTTGAGCTGG
39155_at	4719	ACACACAGCTCATATGCTGCATTCTG
39155_at	4720	CACACAGCTCATATGCTGCATTCTG
39155_at	4721	ACAGCTCATATGCTGCATTCTG
39155_at	4722	GCTCATATGCTGCATTCTG
39155_at	4723	CTCATATGCTGCATTCTG
39155_at	4724	AGGATAGTTCTGTGTACTCCTTTAG
39155_at	4725	GATAGTTCTGTGTACTCCTTTAGGG
39155_at	4726	AGTTCTGTGTACTCCTTTAGGGAGT
39155_at	4727	ACTAGAACTGGGATGTCTTGGCTTG
39155_at	4728	CTAGAACTGGGATGTCTTGGCTTGT
39708_at	4729	TTGTTGTTCTTAGACAAGTGCCTCC
39708_at	4730	TATAGCTACATACTCCTGGCATTGC
39708_at	4731	ATAGCTACATACTCCTGGCATTGCA
39708_at	4732	TAGCTACATACTCCTGGCATTGCAC
39708_at	4733	GCTACATACTCCTGGCATTGCACTT
39708_at	4734	CCTGGCATTGCACTTTTTAACCTTG
39708_at	4735	CTGGCATTGCACTTTTTAACCTTGC
39708_at	4736	TGGCATTGCACTTTTTAACCTTGCT
39708_at	4737	GCATTGCACTTTTTAACCTTGCTGA
39708_at	4738	CCTTGCTGACATCCAAATAGAAGAT
39708_at	4739	CTTGCTGACATCCAAATAGAAGATA
39708_at	4740	TTGCTGACATCCAAATAGAAGATAG
39708_at	4741	TGCTGACATCCAAATAGAAGATAGG
39708_at	4742	GCTGACATCCAAATAGAAGATAGGA
39708_at	4743	GATAGGACTATCTAAGCCCTAGGTT
39708_at	4744	ATAGGACTATCTAAGCCCTAGGTTT
40018_at	4745	CTTCATTGGATAACTTGAAGGCTTT
40018_at	4746	TGACAGTTCCTCATCTTTGAGATG
40018_at	4747	CAGTTCCTCATCTTTGAGATGCAC
40018_at	4748	CATCTTTGAGATGCACTGATCACTG
40018_at	4749	CTTTGAGATGCACTGATCACTGTGC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40018_at	4750	GATGCACTGATCACTGTGCTTGAAA
40018_at	4751	GCACTGATCACTGTGCTTGAAAAAG
40018_at	4752	CTGATCACTGTGCTTGAAAAAGACA
40018_at	4753	ATCACTGTGCTTGAAAAAGACAATA
40018_at	4754	AGGATGACTAATCGTTCTGCTTCTG
40018_at	4755	ACTAATCGTTCTGCTTCTGAGTACA
40018_at	4756	CGTTCTGCTTCTGAGTACATTTTCC
40018_at	4757	TCTGTCAAGGTACACAGCGGTGCCT
40018_at	4758	GTCAAGGTACACAGCGGTGCCTTTG
40018_at	4759	CACAGCGGTGCCTTTGTAAATG TTC
40018_at	4760	AGCGGTGCCTTTGTAAATG TTCATT
40076_at	4761	GTGCTGCCTTTGCATGGGCCTGGCC
40076_at	4762	TCTTTTCTCAGGAGCTACAAAGAT
40076_at	4763	CTCCACACACGACAGAGATGCAGGG
40076_at	4764	CCACACACGACAGAGATGCAGGGGGC
40076_at	4765	ACACACGACAGAGATGCAGGGGGCCA
40076_at	4766	TTGTGCGGGTGTTGACCGATGTATC
40076_at	4767	TGTGCGGGTGTTGACCGATGTATCT
40076_at	4768	GTGCGGGTGTTGACCGATGTATCTT
40076_at	4769	GGTGTTGACCGATGTATCTTTTCCT
40076_at	4770	GTGTTGACCGATGTATCTTTTCCTT
40076_at	4771	GTTGACCGATGTATCTTTTCCTTAA
40076_at	4772	TGACCGATGTATCTTTTCCTTAAAG
40076_at	4773	GACCGATGTATCTTTTCCTTAAAGT
40076_at	4774	TTTGTCAATAAAGCATTTCCTTTGGG
40076_at	4775	TTGTCAATAAAGCATTTCCTTTGGGG
40076_at	4776	GTCAATAAAGCATTTCCTTTGGGGGA
40167_s_at	4777	TGACTTTAGCTGATACTCTTATGTA
40167_s_at	4778	TAGCTGATACTCTTATGTACGAGAT
40167_s_at	4779	ATACTCTTATGTACGAGATCTGTCT
40167_s_at	4780	ACGAGATCTGTCTCTGCTGTTTAAC
40167_s_at	4781	TCTGCTGTTTAACTTCATTGGATTA
40167_s_at	4782	AATCAGCTGGTTTCAACTCTACTGC
40167_s_at	4783	CTGGTTTCAACTCTACTGCGAAACA

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40167_s_at	4784	GGTTTCAACTCTACTGCGAAACAAA
40167_s_at	4785	ATTCTTTAGCTTTCTTAATCGGTGC
40167_s_at	4786	ATGGAGGCCAGTGTAACGTTACATG
40167_s_at	4787	GTAACGTTACATGACTCGTTGAGAA
40167_s_at	4788	CGTTACATGACTCGTTGAGAAAGTT
40167_s_at	4789	CTACCACCTTTGTTGCTTGAAGAAA
40167_s_at	4790	TACCACCTTTGTTGCTTGAAGAAAA
40167_s_at	4791	TGTCTTTTCAAAATGAGAGGCTTTC
40167_s_at	4792	TCTTTTCAAAATGAGAGGCTTTCAT
40177_at	4793	ATATTATACTTTAGGGCAACCCTAG
40177_at	4794	TACTTTAGGGCAACCCTAGTTGGCA
40177_at	4795	TTAGGGCAACCCTAGTTGGCAGCTT
40177_at	4796	TAGGGCAACCCTAGTTGGCAGCTTT
40177_at	4797	AGGGCAACCCTAGTTGGCAGCTTTG
40177_at	4798	GGCAACCCTAGTTGGCAGCTTTGAG
40177_at	4799	ACCCTAGTTGGCAGCTTTGAGAGAA
40177_at	4800	CCCTAGTTGGCAGCTTTGAGAGAAG
40177_at	4801	CCTAGTTGGCAGCTTTGAGAGAAGT
40177_at	4802	TTGGCAGCTTTGAGAGAAGTTCTTC
40177_at	4803	TTCCATTAAACATGGAAGGAATAAC
40177_at	4804	AATAGGGAACCTTGACAGCAGACAGA
40177_at	4805	ATAGGGAACCTTGACAGCAGACAGAG
40177_at	4806	GGAACCTTGACAGCAGACAGAGGGAA
40177_at	4807	GAACCTTGACAGCAGACAGAGGGAAAG
40177_at	4808	ACTTGACAGCAGACAGAGGGAAAGAG
40610_at	4809	ATTTTTCACATATAAGTGGGCTAAC
40610_at	4810	TTTCACATATAAGTGGGCTAACCAA
40610_at	4811	AACTAGCCCTTAATTATGGTGACAG
40610_at	4812	CCCTTAATTATGGTGACAGTTCCTT
40610_at	4813	GAGATTACTCTAGCAACTATTACAG
40610_at	4814	AATTATTTGGTGTGGCCATCTTACC
40610_at	4815	TTGGTGTGGCCATCTTACCTGCTT
40610_at	4816	TTGGTGTGGCCATCTTACCTGCTTA
40610_at	4817	GGCCATCTTACCTGCTTATGTCTCC

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
40610_at	4818	CATCTTACTGTTGATATATGTATGC
40610_at	4819	TCTTACTGTTGATATATGTATGCTC
40610_at	4820	TATATGTATGCTCTGGTACACAGAT
40610_at	4821	GCTCTGGTACACAGATGTCATTTTG
40610_at	4822	GTACACAGATGTCATTTTGTTGTCA
40610_at	4823	CAGATGTCATTTTGTTGTACAGCA
40610_at	4824	TCATTTTGTTGTACAGCACTACAG
41220_at	4825	TGCCAAAACCAAGATTTTGAAGGAA
41220_at	4826	TGTGGCCTGCCAGCCTCAATGTCA
41220_at	4827	CAGCAGCATCCCAGCCTTGAGATGC
41220_at	4828	CCCAGCCTTGAGATGCTTCACTTTC
41220_at	4829	GCCTTGAGATGCTTCACTTTCCTTC
41220_at	4830	TCTGTAACCAGACTTTGAAAAATTG
41220_at	4831	CTGTAACCAGACTTTGAAAAATTGT
41220_at	4832	TAACCAGACTTTGAAAAATTGTTCTG
41220_at	4833	AAATTGTTTCGTTTCATCAGGCTCTG
41220_at	4834	GTTTCGTTTCATCAGGCTCTGTTCT
41220_at	4835	TCATCAGGCTCTGTTCTCTCAATGGC
41220_at	4836	TCAGGCTCTGTTCTCTCAATGGCCTT
41220_at	4837	TCCTCAATGGCCTTTTGCTACGTGC
41220_at	4838	CCTTTTGCTACGTGCCTCCCGAGAA
41220_at	4839	TTGCTACGTGCCTCCCGAGAAATTT
41220_at	4840	TGCCTCCCGAGAAATTTGTCTTTTT
41506_at	4841	ATGCAGGAGGCTTGGAAGTATAACC
41506_at	4842	ATGCAAACTCCTAAGAGATACTCTG
41506_at	4843	AAGAGATACTCTGCAGAGCTTCAGC
41506_at	4844	GCAGAGCTTCAGCTGGAATGGTCGT
41506_at	4845	CTTCAGCTGGAATGGTCGTGGATTTC
41506_at	4846	AGCTGGAATGGTCGTGGATTTCACAG
41506_at	4847	TAGAAGAGCAAACCACGTCCACGA
41506_at	4848	AAGAGCAAACCACGTCCACGAATC
41506_at	4849	CGAATCCCAATAATGACAGCTTCAG
41506_at	4850	CCAATAATGACAGCTTCAGACTTTG
41506_at	4851	ATAATGACAGCTTCAGACTTTGTTT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
41506_at	4852	CACTTGCCAGCAGTAGAAAAAGGAC
41506_at	4853	CTTGCCAGCAGTAGAAAAAGGACCG
41506_at	4854	TTGCCAGCAGTAGAAAAAGGACCGA
41506_at	4855	AGGACCGACTATACCGACCTTTCTG
41506_at	4856	CCGACCTTTCTGATTAGTAAACAGT
41604_at	4857	AAAGGCACCTAAGCTATTGCTAATT
41604_at	4858	ACCTAAGCTATTGCTAATTGAATTG
41604_at	4859	CTATGTATCTAGTATTGAGGCTTGC
41604_at	4860	ATGTATCTAGTATTGAGGCTTGCTC
41604_at	4861	TTGAGGCTTGCTCTTTCATGTGGCT
41604_at	4862	CTTGCTCTTTCATGTGGCTTTATCC
41604_at	4863	TGCTCTTTCATGTGGCTTTATCCTC
41604_at	4864	TGTGGCTTTATCCTCTCTTTAATAG
41604_at	4865	GTGGCTTTATCCTCTCTTTAATAGC
41604_at	4866	CTTCAGGATCAGCTTGCAGAGTCTT
41604_at	4867	GATCAGCTTGCAGAGTCTTGCTTTT
41604_at	4868	ATCAGCTTGCAGAGTCTTGCTTTTA
41604_at	4869	CTTGCAGAGTCTTGCTTTTAGGTTA
41604_at	4870	TCTTGCTTTTAGGTTAGATACAAAC
41604_at	4871	AACAGCTGGCTTTGGAATGGAGAAC
41604_at	4872	AGCTGGCTTTGGAATGGAGAACT
41787_at	4873	GGAATCGTGGCAATTTCTCTTAGAA
41787_at	4874	CGTGGCAATTTCTCTTAGAAAGTAG
41787_at	4875	GTGACTACCTGTACAGTTGCACTAT
41787_at	4876	GTACAGTTGCACTATGTTCTTCATA
41787_at	4877	ATACAAAATTTACATTCAAGCTGGG
41787_at	4878	TACAAAATTTACATTCAAGCTGGGT
41787_at	4879	AAATTTACATTCAAGCTGGGTCTTT
41787_at	4880	TTACATTCAAGCTGGGTCTTTACTA
41787_at	4881	ATTCAAGCTGGGTCTTTACTACTGA
41787_at	4882	GCTGGGTCTTTACTACTGAAAATAA
41787_at	4883	GAAATATGCCAGGATTCTTTTGTTTC
41787_at	4884	AATATGCCAGGATTCTTTTGTTCAA
41787_at	4885	CATTACACAGCTTTGCTTCTTTGGT

Qualifier	SEQ ID NO	Oligonucleotide Probe (from 5' to 3')
41787_at	4886	ACAGCTTTGCTTCTTTGGTTACAAA
41787_at	4887	GCTTTGCTTCTTTGGTTACAAAGTA
41787_at	4888	CTTTGCTTCTTTGGTTACAAAGTAG
649_s_at	4889	AGGGTCCAGCCTCAAGATCCTCTCC
649_s_at	4890	CCTCAAGATCCTCTCCAAAGGAAAG
649_s_at	4891	CCTCTCCAAAGGAAAGCGAGGTGGA
649_s_at	4892	CATTCATCTGTTTCCACTGAGTCTG
649_s_at	4893	GTTTCCACTGAGTCTGAGTCTTCAA
649_s_at	4894	GAGTCTGAGTCTTCAAGTTTTCACT
649_s_at	4895	TTCAAGTTTTCACTCCAGCTAACAC
649_s_at	4896	GTGTGTCTAGGCAGGACCTGTGGCC
649_s_at	4897	ATCACGTAAAGCTAGAAATGATCCC
649_s_at	4898	TGATCCCCAGCTGTTTATGCATAGA
649_s_at	4899	TGCATAGATAATCTCTCCATTCCCG
649_s_at	4900	AGACGTGATTTTGCTGTAGAAGATG
649_s_at	4901	AGATGGCACTTATAACCAAAGCCCA
649_s_at	4902	ATGCTGGTTTTTCAGTTTTTCAGGAG
649_s_at	4903	TGATTTTCAGCACCTACAGTGTACAG
649_s_at	4904	CACCTACAGTGTACAGTCTTGTATT